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 ttgcttgtgt cccagggcgg cactaaccag aaccagaaaa ggaaatcttt ggcctcggg 240
 gagaattatg ccaattatct gtctggttcc tgtctttgaa aatgccaga tgttggttta 300
 caaatcagga agctgtcttg gggcaatctc tgttccctct ttgatgcaga gagcctttct 360
 ctgtaaacac tggagagcag ggcttcactg tctggctccc ctccgcctc ttgcaggaag 420
 gactagatgc tgctgatcag ctgatcatgg ctgagccggg tagagcttgg ggctctccta 480
 agaggtcacc cactgggagg gagcttcaca gctgttcttt tgaccagga aggagctctt 540
 tcaggactgt ggcaccagga gccgtggccc tctgcc atg cca ttg ttc cca ctt 595

Met Pro Leu Phe Pro Leu
1 5

ccc tgc cct tgg gag tct tgg aga cag ctg act agc tgc cct gag ggg 643
Pro Cys Pro Trp Glu Ser Trp Arg Gln Leu Thr Ser Cys Pro Glu Gly
10 15 20

tcc acc gct ctc acc ttc tca ctg gtg gct gct gcc att ctc ctg ggc 691
Ser Thr Ala Leu Thr Phe Ser Leu Val Ala Ala Ala Ile Leu Leu Gly
25 30 35

tct gca cag aaa gct ttg gtc ctt ctg aaa gcc act ctg ccc ctt cct 739
Ser Ala Gln Lys Ala Leu Val Leu Leu Lys Ala Thr Leu Pro Leu Pro
40 45 50

gca gca cca gat ccc cct gag ccg gta ctg ctg cct cca cct ggg cca 787
Ala Ala Pro Asp Pro Pro Glu Pro Val Leu Leu Pro Pro Pro Gly Pro
55 60 65 70

aga cta gtc ttg gtg ttc acc ctt ctt cgt gct tca gaa agt agg gat 835
Arg Leu Val Leu Val Phe Thr Leu Leu Arg Ala Ser Glu Ser Arg Asp
75 80 85

atc tgg gga cat gac tgt gtt tcc ctg ggg tcc ttt cag aag aga ctt 883
Ile Trp Gly His Asp Cys Val Ser Leu Gly Ser Phe Gln Lys Arg Leu
90 95 100

agg aag ctc ctg ctc agg aat ctg gcc ctc tga aagagccc cttcaaagca 934
Arg Lys Leu Leu Arg Asn Leu Ala Leu *
105 110

gcctgggcag caggtaacgt ggtttccctt gcggccccct cctcccagct gcatagactc 994

gtgggtttgaa gtgaacagat cttgtccgga ac 1026

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Met Val Val Gly Ala Phe Pro Met Ala Lys Leu Leu Tyr
1 5 10

ttg ggc atc cgg cag gtc agc aag ccg ctt gcc aac cgt att aag gag 156
Leu Gly Ile Arg Gln Val Ser Lys Pro Leu Ala Asn Arg Ile Lys Glu
15 20 25

gcc gcc cgc cga agc gag ttc ttc aag acc tat atc tgc ctc ccg ccg	204
Ala Ala Arg Arg Ser Glu Phe Phe Lys Thr Tyr Ile Cys Leu Pro Pro	
30 35 40 45	
gct caa ctg tat cac tgg gtg gag atg cgg acc aag atg cgc atc atg	252
Ala Gln Leu Tyr His Trp Val Glu Met Arg Thr Lys Met Arg Ile Met	
50 55 60	
ggc ttc cgg ggc acg gtc atc aag ccg ctg aac gag gag gcg gca gct	300
Gly Phe Arg Gly Thr Val Ile Lys Pro Leu Asn Glu Glu Ala Ala Ala	
65 70 75	
gag ctg ggc gca gag ctg ctg ggc gaa gcc acc atc ttc atc gtg ggc	348
Glu Leu Gly Ala Glu Leu Leu Gly Glu Ala Thr Ile Phe Ile Val Gly	
80 85 90	
ggc ggc tgc cta gtg ctg gag tac tgg cgc cac cag gcg cag cag cgc	396
Gly Gly Cys Leu Val Leu Glu Tyr Trp Arg His Gln Ala Gln Gln Arg	
95 100 105	
cac aag gag gag gag cag cgt gct gcc tgg aac gcg ctg cgg gac gag	444
His Lys Glu Glu Glu Gln Arg Ala Ala Trp Asn Ala Leu Arg Asp Glu	
110 115 120 125	
gtg ggc cac ctg gcg ctg gcg ctg gaa gcg ctg cag gcg cag gtg cag	492
Val Gly His Leu Ala Leu Ala Leu Glu Ala Leu Gln Ala Gln Val Gln	
130 135 140	
gcg gcg ccg cca cag ggc gcc ctg gag gaa ctg cgc aca gag ctg caa	540
Ala Ala Pro Pro Gln Gly Ala Leu Glu Glu Leu Arg Thr Glu Leu Gln	
145 150 155	
gag gtg cgc gcc cag ctc tgc aat ccc ggc cgg tcc gct tcc cac gca	588
Glu Val Arg Ala Gln Leu Cys Asn Pro Gly Arg Ser Ala Ser His Ala	
160 165 170	
gtg cct gcg tcc aag aaa tag ga gcttgctgga tggaacctga atttgacat	641
Val Pro Ala Ser Lys Lys *	
175 180	
ggcctatgta cctaactgtg ccttcttccc gcaccacct tgacctgcgct ggcccagtgg	701
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cgctcccccg gaccatcgg cgcgctgccc acacctccag gcgaccggcc aactgggtcc 480
tgaagtagct gaa atg cga aaa agg cag cag tcc caa aat gaa gga aca 529
Met Arg Lys Arg Gln Gln Ser Gln Asn Glu Gly Thr
1 5 10
cct gcc gtg tct caa gct cct gga aac cag agg ccc aac aac acc tgt 577
Pro Ala Val Ser Gln Ala Pro Gly Asn Gln Arg Pro Asn Asn Thr Cys
15 20 25
tgc ttt tgt tgg tgc tgt tgt tgc agc tgc tcc tgc ctc act gtg agg 625
Cys Phe Cys Trp Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg
30 35 40
aat gaa gaa aga ggg gaa aat gcg gga aga ccc aca cac act aca aaa 673
Asn Glu Glu Arg Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys
45 50 55 60
atg gag agt atc cag gtc cta gag gaa tgc caa aac ccc act gca gag 721
Met Glu Ser Ile Gln Val Leu Glu Glu Cys Gln Asn Pro Thr Ala Glu
65 70 75
gaa gtc ttg tcc tgg tct caa aat ttt gac aag atg atg aag gcc cca 769
Glu Val Leu Ser Trp Ser Gln Asn Phe Asp Lys Met Met Lys Ala Pro

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Ala Gly Arg Asn Leu Phe Arg Glu Phe Leu Arg Thr Glu Tyr Ser Glu			
95	100	105	
gag aac cta ctt ttc tgg ctt gct tgt gaa gac tta aag aag gag cag			865
Glu Asn Leu Leu Phe Trp Leu Ala Cys Glu Asp Leu Lys Lys Glu Gln			
110	115	120	
aac aaa aaa gta att gaa gaa aag gct agg atg ata tat gaa gat tac			913
Asn Lys Lys Val Ile Glu Glu Lys Ala Arg Met Ile Tyr Glu Asp Tyr			
125	130	135	140
att tct ata cta tca cca aaa gag gtc agt ctt gat tct cga gtt aga			961
Ile Ser Ile Leu Ser Pro Lys Glu Val Ser Leu Asp Ser Arg Val Arg			
145	150	155	
gag gtg atc aat aga aat ctg ttg gat ccc aat cct cac atg tat gaa			1009
Glu Val Ile Asn Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu			
160	165	170	
gat gcc caa ctt cag ata tat act tta atg cac aga gat tct ttt cca			1057
Asp Ala Gln Leu Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro			
175	180	185	
agg ttt ttg aac tct caa att tat aag tca ttt gtt gaa agt act gct			1105
Arg Phe Leu Asn Ser Gln Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala			
190	195	200	
ggc tct tct tct gaa tct taa tg ttcatttaaa aacaatcatt ttggagggt			1158
Gly Ser Ser Ser Glu Ser *			
205	210		
gagatgggaa ataaaagtag ttaaataaca tcagaaactg agttcctgga gaactacagt			1218
ttagcattcc tcaggctact gtgaaaacac aaccgttatg gtctttgtct ccatttttat			1278
caaggttttc catgggtaag tttggagaaa ataccacaca aaacaatgaa ttgccaaatt			1338
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agacagagct gtgaaccaac cccgctcacg gctaacaagc ccacccacc      atg gcg      175
                                   Met Ala
                                   1
agc ccc act ctg agc ccc gac tcc tca tcc cag gag gcc ctg tcg gcc      223
Ser Pro Thr Leu Ser Pro Asp Ser Ser Ser Gln Glu Ala Leu Ser Ala
                    5                      10                      15

ccc acc tgc tcc cca acc tct gac tcc gag aac ctc agc ccc gat gag      271
Pro Thr Cys Ser Pro Thr Ser Asp Ser Glu Asn Leu Ser Pro Asp Glu
                    20                      25                      30

ctg gag ctg ctg gcc aag ctc gaa gag cag aac cgg ctc ctg gag gcc      319
Leu Glu Leu Leu Ala Lys Leu Glu Glu Gln Asn Arg Leu Leu Glu Ala
                    35                      40                      45                      50

gac tcc aag tcc atg cgc tcc atg aat ggc tcg cgg cgg aac agt ggc      367
Asp Ser Lys Ser Met Arg Ser Met Asn Gly Ser Arg Arg Asn Ser Gly
                    55                      60                      65

tcc tcg cta gtg tcc agc tcc tcg gcc tcc tcc aac ctg agc cac ctg      415
Ser Ser Leu Val Ser Ser Ser Ser Ala Ser Ser Asn Leu Ser His Leu
                    70                      75                      80

gag gag gac acg tgg atc ctg tgg ggc cgg atc gcc aac gag tgg gag      463
Glu Glu Asp Thr Trp Ile Leu Trp Gly Arg Ile Ala Asn Glu Trp Glu
                    85                      90                      95

gag tgg cgg cgc agg aag gag aag ctg ctc aag gag ctg atc cgc aag      511
Glu Trp Arg Arg Arg Lys Glu Lys Leu Leu Lys Glu Leu Ile Arg Lys
                    100                      105                      110

ggc atc ccc cac cac ttc cgg gcc atc gtg tgg cag ctt ctg tgc agc      559
Gly Ile Pro His His Phe Arg Ala Ile Val Trp Gln Leu Leu Cys Ser
                    115                      120                      125                      130

gcc acg gac atg ccc gtc aag aac cag tac tcc gag ctg ctc aag atg      607
Ala Thr Asp Met Pro Val Lys Asn Gln Tyr Ser Glu Leu Leu Lys Met
                    135                      140                      145

tcc tcg ccg tgc gag aag ctg atc cgc agg gac atc gcc cgc acc tac      655

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Ser	Ser	Pro	Cys	Glu	Lys	Leu	Ile	Arg	Arg	Asp	Ile	Ala	Arg	Thr	Tyr	
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ccg	gaa	cac	gag	ttc	ttc	aag	ggc	cag	gac	agc	ctg	ggc	cag	gag	gtc	703
Pro	Glu	His	Glu	Phe	Phe	Lys	Gly	Gln	Asp	Ser	Leu	Gly	Gln	Glu	Val	
		165					170					175				
ctc	ttc	aac	gtc	atg	aag	gca	tac	tcg	ctg	gta	gac	cgg	gag	gtg	ggc	751
Leu	Phe	Asn	Val	Met	Lys	Ala	Tyr	Ser	Leu	Val	Asp	Arg	Glu	Val	Gly	
	180					185					190					
tac	tgc	cag	gga	agc	gcc	ttc	atc	gtg	ggc	ctg	ctc	ctc	atg	cag	atg	799
Tyr	Cys	Gln	Gly	Ser	Ala	Phe	Ile	Val	Gly	Leu	Leu	Leu	Met	Gln	Met	
195					200					205					210	
cct	gag	gag	gag	gcc	ttc	tgt	gtg	ttc	gtg	cgg	ctg	atg	cag	gag	tac	847
Pro	Glu	Glu	Glu	Ala	Phe	Cys	Val	Phe	Val	Arg	Leu	Met	Gln	Glu	Tyr	
				215					220					225		
cgg	ctg	cgg	gag	ctc	ttc	aaa	ccc	agc	atg	gcc	gag	ctc	ggg	ctc	tgc	895
Arg	Leu	Arg	Glu	Leu	Phe	Lys	Pro	Ser	Met	Ala	Glu	Leu	Gly	Leu	Cys	
			230					235					240			
atc	tat	cag	ttc	gag	tac	atg	ctg	cag	gag	cag	ctc	cca	gac	ctc	aac	943
Ile	Tyr	Gln	Phe	Glu	Tyr	Met	Leu	Gln	Glu	Gln	Leu	Pro	Asp	Leu	Asn	
		245					250					255				
acc	cac	ttc	cgt	tcc	caa	agc	ttc	cac	aca	tcc	atg	tat	gcc	tcg	tcc	991
Thr	His	Phe	Arg	Ser	Gln	Ser	Phe	His	Thr	Ser	Met	Tyr	Ala	Ser	Ser	
	260					265					270					
tgg	ttc	ctc	aca	ctg	ttc	ctg	acc	acc	ttc	cca	ctc	ccc	gtc	gcc	acc	1039
Trp	Phe	Leu	Thr	Leu	Phe	Leu	Thr	Thr	Phe	Pro	Leu	Pro	Val	Ala	Thr	
275					280					285					290	
cgg	gtc	ttt	gac	atc	ttc	atg	tat	gag	ggg	ctg	gag	atc	gtg	ttc	cga	1087
Arg	Val	Phe	Asp	Ile	Phe	Met	Tyr	Glu	Gly	Leu	Glu	Ile	Val	Phe	Arg	
			295						300					305		
gtg	ggc	ctc	gcc	ctg	ctg	cag	gtg	aac	cag	gcg	gag	ctg	atg	cag	ctg	1135
Val	Gly	Leu	Ala	Leu	Leu	Gln	Val	Asn	Gln	Ala	Glu	Leu	Met	Gln	Leu	
			310					315					320			
gac	atg	gag	ggg	atg	tcc	cag	tac	ttc	cag	aga	gtg	atc	ccc	cac	cag	1183
Asp	Met	Glu	Gly	Met	Ser	Gln	Tyr	Phe	Gln	Arg	Val	Ile	Pro	His	Gln	
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ttc	gac	agc	tgc	ccg	gac	aag	ctg	gtc	ctc	aaa	gcc	tac	cag	gtc	aag	1231
Phe	Asp	Ser	Cys	Pro	Asp	Lys	Leu	Val	Leu	Lys	Ala	Tyr	Gln	Val	Lys	
	340					345					350					
tac	aac	ccc	aag	aag	atg	aag	agg	ctg	gag	aag	gag	tac	gca	gcc	atg	1279
Tyr	Asn	Pro	Lys	Lys	Met	Lys	Arg	Leu	Glu	Lys	Glu	Tyr	Ala	Ala	Met	
355					360					365					370	
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Lys	Ser	Lys	Glu	Met	Glu	Glu	Gln	Ile	Glu	Ile	Lys	Arg	Leu	Arg	Thr	

375								380				385				
gag	aac	cgg	ctc	ctg	aaa	cag	cgg	att	gaa	acc	cta	gag	aag	gag	agc	1375
Glu	Asn	Arg	Leu	Leu	Lys	Gln	Arg	Ile	Glu	Thr	Leu	Glu	Lys	Glu	Ser	
			390						395			400				
gct	gct	ctg	gct	gat	agg	tta	atc	cag	ggg	caa	gtg	aca	cgg	gcg	cag	1423
Ala	Ala	Leu	Ala	Asp	Arg	Leu	Ile	Gln	Gly	Gln	Val	Thr	Arg	Ala	Gln	
			405						410			415				
gag	gcg	gag	gag	aac	tac	gtc	atc	aag	cgg	gag	ctg	gcg	gtg	gtg	cgg	1471
Glu	Ala	Glu	Glu	Asn	Tyr	Val	Ile	Lys	Arg	Glu	Leu	Ala	Val	Val	Arg	
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cag	cag	tgc	agc	tcg	gcg	gcc	gag	gac	ctg	cag	aag	gca	cag	agc	acc	1519
Gln	Gln	Cys	Ser	Ser	Ala	Ala	Glu	Asp	Leu	Gln	Lys	Ala	Gln	Ser	Thr	
			435						440			445			450	
atc	cgg	cag	cta	cag	gag	cag	cag	gag	aac	ccc	cgc	ctc	aca	gaa	gac	1567
Ile	Arg	Gln	Leu	Gln	Glu	Gln	Gln	Glu	Asn	Pro	Arg	Leu	Thr	Glu	Asp	
			455						460			465				
ttc	gtg	tcc	cac	ctg	gag	acc	gag	ctg	gag	cag	tcg	agg	ctg	cgg	gag	1615
Phe	Val	Ser	His	Leu	Glu	Thr	Glu	Leu	Glu	Gln	Ser	Arg	Leu	Arg	Glu	
			470						475			480				
acg	gag	aca	ctg	ggg	gcc	ctt	cgg	gag	atg	cag	gac	aag	gtt	ctc	gac	1663
Thr	Glu	Thr	Leu	Gly	Ala	Leu	Arg	Glu	Met	Gln	Asp	Lys	Val	Leu	Asp	
			485						490			495				
atg	gaa	aag	agg	aac	agc	tcg	ctg	ccc	gac	gag	aac	aat	gtg	gcg	cag	1711
Met	Glu	Lys	Arg	Asn	Ser	Ser	Leu	Pro	Asp	Glu	Asn	Asn	Val	Ala	Gln	
			500						505			510				
ctg	cag	gag	gag	ctg	aag	gcg	ctc	aag	gtg	cgg	gaa	ggc	cag	gcg	gtg	1759
Leu	Gln	Glu	Glu	Leu	Lys	Ala	Leu	Lys	Val	Arg	Glu	Gly	Gln	Ala	Val	
			515						520			525			530	
gcc	tcg	acg	cga	gag	ctt	aaa	ctg	cag	ctg	cag	gag	ctc	tcg	gac	acc	1807
Ala	Ser	Thr	Arg	Glu	Leu	Lys	Leu	Gln	Leu	Gln	Glu	Leu	Ser	Asp	Thr	
			535						540			545				
tgg	cag	gac	cag	atc	gag	gag	ctg	aag	acc	gag	gtg	cgg	ctg	ctg	aag	1855
Trp	Gln	Asp	Gln	Ile	Glu	Glu	Leu	Lys	Thr	Glu	Val	Arg	Leu	Leu	Lys	
			550						555			560				
ggc	ccg	ccg	ccc	ttc	gag	gac	ccg	ctg	gct	ttc	gat	ggg	ctg	agc	ctg	1903
Gly	Pro	Pro	Pro	Phe	Glu	Asp	Pro	Leu	Ala	Phe	Asp	Gly	Leu	Ser	Leu	
			565						570			575				
gcg	cgg	cac	ttg	gac	gag	gac	tcg	ctg	ccg	tcg	tcg	gac	gag	gag	cta	1951
Ala	Arg	His	Leu	Asp	Glu	Asp	Ser	Leu	Pro	Ser	Ser	Asp	Glu	Glu	Leu	
			580						585			590				
ctt	ggc	gta	ggc	gtg	ggc	gct	gcc	ctg	cag	gac	gca	ttg	tac	cct	ctg	1999
Leu	Gly	Val	Gly	Val	Gly	Ala	Ala	Leu	Gln	Asp	Ala	Leu	Tyr	Pro	Leu	
			595						600			605			610	

tcc ccg cgc gat gcg cgc ttc ttc cgc cgt ctg gag cgg ccg gcc aag	2047
Ser Pro Arg Asp Ala Arg Phe Phe Arg Arg Leu Glu Arg Pro Ala Lys	
615 620 625	
gac agc gag ggc agc tca gac agc gac gcc gat gag ctg gcc gcg ccc	2095
Asp Ser Glu Gly Ser Ser Asp Ser Asp Ala Asp Glu Leu Ala Ala Pro	
630 635 640	
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Tyr Ser Gln Gly Leu Asp Asn *	
645 650	
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gagggtaggg tccgacctgg gctcctcagg gccccggggc aggctctctc tccccagcag	2329
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gctctccaca cgccccctac actgccgcc accattttgc aactgcctg ttcacatgtc	3349
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<400> 228

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agcagcgagg acacctgcag aaatacattc ccaaagcaag gctgggcggc cgtgtgaagt    180
aagcaatggc ctcaagttttg cttctgtttt ggatgaacac caccacatag ggcctgaatg    240
tgaaagaaga ccctctatatt gtctgttccg gggcagcctg gtagtaaaac actgttgaat    300
gggccacagt ttcagcagac catcaggtga      atg gga cca gtc tct ctt ctt    351
                                   Met Gly Pro Val Ser Leu Leu
                                   1               5

cca aaa tat cag aag tta aac act tgg aac gga gat ttg gcc aag atg      399
Pro Lys Tyr Gln Lys Leu Asn Thr Trp Asn Gly Asp Leu Ala Lys Met
              10                15                20

acc cat tta cag gct gga ctc agt cca gag act ata gag aaa gct cgc      447
Thr His Leu Gln Ala Gly Leu Ser Pro Glu Thr Ile Glu Lys Ala Arg
              25                30                35

ctg gaa ctg aat gaa aac ccc gat gtt tta cat cag gat att cag caa      495
Leu Glu Leu Asn Glu Asn Pro Asp Val Leu His Gln Asp Ile Gln Gln
              40                45                50                55

gtc agg gac atg atc atc acc agg cct gac att gga ttt tta cgt aca      543
Val Arg Asp Met Ile Ile Thr Arg Pro Asp Ile Gly Phe Leu Arg Thr
              60                65                70

gat gat gcc ttc atc ctg aga ttt ctc cga gcc agg aag ttt cac caa      591
Asp Asp Ala Phe Ile Leu Arg Phe Leu Arg Ala Arg Lys Phe His Gln
              75                80                85

gcg gat gcc ttt aga ctc ctg gct cag tat ttc cag tac cgc cag cta      639
Ala Asp Ala Phe Arg Leu Leu Ala Gln Tyr Phe Gln Tyr Arg Gln Leu
              90                95                100

aac ctg gac atg ttc aaa aac ttc aag gca gat gat ccc ggc att aag      687
Asn Leu Asp Met Phe Lys Asn Phe Lys Ala Asp Asp Pro Gly Ile Lys
              105                110                115

agg gct ctg atc gat ggg ttc ccc ggg gtg ctg gaa aac cga gac cat      735
Arg Ala Leu Ile Asp Gly Phe Pro Gly Val Leu Glu Asn Arg Asp His
              120                125                130                135

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tac ggc agg aag att ctt ttg ctg ttt gca gcc aat tgg gat cag agt	783
Tyr Gly Arg Lys Ile Leu Leu Leu Phe Ala Ala Asn Trp Asp Gln Ser	
140 145 150	
agg aac tcc ttc aca gac atc ctt cgt gcc atc ctg ctg tca ttg gaa	831
Arg Asn Ser Phe Thr Asp Ile Leu Arg Ala Ile Leu Leu Ser Leu Glu	
155 160 165	
gtc cta atc gaa gat ccg gag ctt cag ata aat ggc ttc att tta att	879
Val Leu Ile Glu Asp Pro Glu Leu Gln Ile Asn Gly Phe Ile Leu Ile	
170 175 180	
ata gac tgg agt aat ttt tcc ttc aaa caa gcc tcc aaa ctg aca cct	927
Ile Asp Trp Ser Asn Phe Ser Phe Lys Gln Ala Ser Lys Leu Thr Pro	
185 190 195	
tca atc ctt aaa ctg gcc att gaa ggg ttg cag gac agc ttt cct gcc	975
Ser Ile Leu Lys Leu Ala Ile Glu Gly Leu Gln Asp Ser Phe Pro Ala	
200 205 210 215	
cgc ttt gga gga gtc cac ttt gtc aac cag ccc tgg tac att cat gcc	1023
Arg Phe Gly Gly Val His Phe Val Asn Gln Pro Trp Tyr Ile His Ala	
220 225 230	
ctc tac aca ctc atc aag cca ttt ctt aaa gac aag acc agg aaa cgg	1071
Leu Tyr Thr Leu Ile Lys Pro Phe Leu Lys Asp Lys Thr Arg Lys Arg	
235 240 245	
att ttc ctg cat gga aac aat tta aac agc ctt cac cag cta ata cac	1119
Ile Phe Leu His Gly Asn Asn Leu Asn Ser Leu His Gln Leu Ile His	
250 255 260	
cct gaa ttt ttg ccc tct gaa ttt gga gga act ctt cct ccc tta tga	1167
Pro Glu Phe Leu Pro Ser Glu Phe Gly Gly Thr Leu Pro Pro Leu *	
265 270 275	
catgggaact tgggcccga cgttactcgg tcccgaactac agcgatgaaa atgactatac	1227
tcacacatcc tataatgcaa tgcacgtgaa gcatacgtcc tcgaatctgg agagagaatg	1287
ctcacccaag ctgatgaaaa gatctcagtc tgtggtagaa gctgggaccc tgaaacatga	1347
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ccccaatgct cctgcacact ggccttcagt ggtatcagcc acccaggaag cacatgcaca	1467
actgaccat gcagacacgt gtgttctgct tgacacaagg tcctccactc ctgaaccct	1527
gcagtgactg tcaccagcca tcggtctgag cagccaaagt tggacaaaga cttgagagat	1587
gctttttttt tccccagtg aggggactgg aggatgatgc aaggcattta tgtaaaaaag	1647
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aaaaaaaaaa aa	1719

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agtcagattc tgactctgca tacccttcca      atg gct ttc gcc acc ccc aaa      171
                                   Met Ala Phe Ala Thr Pro Lys
                                   1              5

tca ctt gga gta aaa gcc gaa gtc ctt cca gca gct tac cag gtg ctg      219
Ser Leu Gly Val Lys Ala Glu Val Leu Pro Ala Ala Tyr Gln Val Leu
      10              15              20

cat gat cca gac tcc ttc tta gcc ctc tgg ctc tcc tgc tgc tct cct      267
His Asp Pro Asp Ser Phe Leu Ala Leu Trp Leu Ser Cys Cys Ser Pro
      25              30              35

tct tca ttt ctc tct agc cac acc agc ttt ctt gct gag agc act ggg      315
Ser Ser Phe Leu Ser Ser His Thr Ser Phe Leu Ala Glu Ser Thr Gly
      40              45              50              55

tgc tct gtc tac act att ctc caa aat atc cat atg gtt tgt cct cct      363
Cys Ser Val Tyr Thr Ile Leu Gln Asn Ile His Met Val Cys Pro Pro
      60              65              70

tca ttt act ttc ttg aat tcc acg gtc tca gtg aga tta cct tgg cat      411
Ser Phe Thr Phe Leu Asn Ser Thr Val Ser Val Arg Leu Pro Trp His
      75              80              85

cct agt taa agctgct gcctgtcctc tcaccctgcg tcctgcagtc ccctttctag      467
Pro Ser *
      90

cgccccctcc ctttttctat agcactcttc aacttctaac atactttttaa aacataattt      527
ccttgatatgt ttgctgag      546

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cagccgccag cgcgccccgt cggcagctct ccattctgcac gtctctccgt gaaccccgtg      180
agcgggtgtgc agccacc      atg ttc agc tgg ctg aag cgg ggc ggg gca cgg      230
                        Met Phe Ser Trp Leu Lys Arg Gly Gly Ala Arg
                        1           5           10

ggc cag cag ccc gag gcc atc cgc acg gtg acc tcg gcc ctc aag gag      278
Gly Gln Gln Pro Glu Ala Ile Arg Thr Val Thr Ser Ala Leu Lys Glu
                        15           20           25

ctg tac cgc acg aag ctg ctg ccg ctg gag gag cac tac cgc ttt ggg      326
Leu Tyr Arg Thr Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe Gly
                        30           35           40

gcc ttc cac tcg ccg gcc ctg gag gac gca gac ttc gac ggc aag ccc      374
Ala Phe His Ser Pro Ala Leu Glu Asp Ala Asp Phe Asp Gly Lys Pro
                        45           50           55

atg gtg ctg gtg gcc ggc cag tac agc acg ggc aag acc agc ttc atc      422
Met Val Leu Val Ala Gly Gln Tyr Ser Thr Gly Lys Thr Ser Phe Ile
                        60           65           70           75

cag tac ctg ctg gag cag gag gtg ccc ggc tcc cgc gtg ggg cct gag      470
Gln Tyr Leu Leu Glu Gln Glu Val Pro Gly Ser Arg Val Gly Pro Glu
                        80           85           90

ccc acc acc gac ttc ttt gtg gcc gtc atg cac ggc gac act gag ggc      518
Pro Thr Thr Asp Phe Phe Val Ala Val Met His Gly Asp Thr Glu Gly
                        95           100           105

acc gtg ccc ggc aac gcc ctc gtc gtg gac ccg gac aag ccc ttc cgc      566
Thr Val Pro Gly Asn Ala Leu Val Val Asp Pro Asp Lys Pro Phe Arg
                        110           115           120

aaa ctc aac cct ttc gga aac acc ttc ctc aac agg ttc atg tgt gcc      614
Lys Leu Asn Pro Phe Gly Asn Thr Phe Leu Asn Arg Phe Met Cys Ala
                        125           130           135

cag ctc cct aat cag gtc ctg gag agc atc agc atc atc gac acc ccg      662
Gln Leu Pro Asn Gln Val Leu Glu Ser Ile Ser Ile Ile Asp Thr Pro
                        140           145           150           155

ggt atc ctg tcg ggt gcc aag cag aga gtg agc cgc ggc tac gac ttc      710
Gly Ile Leu Ser Gly Ala Lys Gln Arg Val Ser Arg Gly Tyr Asp Phe
                        160           165           170

ccg gcc gtg ctg cgc tgg ttc gcg gag cgc gtg gac ctc atc atc ctg      758
Pro Ala Val Leu Arg Trp Phe Ala Glu Arg Val Asp Leu Ile Ile Leu
                        175           180           185

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ctc ttt gat gcg cac aag ctg gag atc tcg gac gag ttc tca gag gcc	806
Leu Phe Asp Ala His Lys Leu Glu Ile Ser Asp Glu Phe Ser Glu Ala	
190 195 200	
atc ggc gcg ttg cgg ggc cat gag gac aag atc cgc gtg gtg ctc aac	854
Ile Gly Ala Leu Arg Gly His Glu Asp Lys Ile Arg Val Val Leu Asn	
205 210 215	
aag gcc gac atg gtg gag acg cag cag ctg atg cgc gtc tac ggc gcg	902
Lys Ala Asp Met Val Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala	
220 225 230 235	
ctc atg tgg gcg ctg ggc aag gtg gtg ggc acg ccc gag gtg ctg cgc	950
Leu Met Trp Ala Leu Gly Lys Val Val Gly Thr Pro Glu Val Leu Arg	
240 245 250	
gtc tac atc ggc tcc ttc tgg tcc cag ccc ctc ctc gtg ccc gac aac	998
Val Tyr Ile Gly Ser Phe Trp Ser Gln Pro Leu Leu Val Pro Asp Asn	
255 260 265	
cgg cgc ctc ttc gag ctg gag gag cag gac ctc ttc cgc gac atc cag	1046
Arg Arg Leu Phe Glu Leu Glu Glu Gln Asp Leu Phe Arg Asp Ile Gln	
270 275 280	
ggc ctg ccc cgg cac gca gcc ttg cgc aag ctc aac gac ctg gtg aag	1094
Gly Leu Pro Arg His Ala Ala Leu Arg Lys Leu Asn Asp Leu Val Lys	
285 290 295	
agg gcc cgg ctg gtg cga gtt cac gct tac atc atc agc tac ctg aag	1142
Arg Ala Arg Leu Val Arg Val His Ala Tyr Ile Ile Ser Tyr Leu Lys	
300 305 310 315	
aag gag atg ccc tct gtg ttt ggg aag gag aac aag aag aag cag ctg	1190
Lys Glu Met Pro Ser Val Phe Gly Lys Glu Asn Lys Lys Lys Gln Leu	
320 325 330	
atc ctc aaa ctg ccc gtc atc ttt gcg aag att cag ctg gaa cat cac	1238
Ile Leu Lys Leu Pro Val Ile Phe Ala Lys Ile Gln Leu Glu His His	
335 340 345	
atc tcc cct ggg gac ttt cct gat tgc cag aaa atg cag gag ctg ctg	1286
Ile Ser Pro Gly Asp Phe Pro Asp Cys Gln Lys Met Gln Glu Leu Leu	
350 355 360	
atg gcg cac gac ttc acc aag ttt cac tcg ctg aag ccg aag ctg cta	1334
Met Ala His Asp Phe Thr Lys Phe His Ser Leu Lys Pro Lys Leu Leu	
365 370 375	
gag gca ctg gac gag atg ctg acg cac gac atc gcc aag ctc atg ccc	1382
Glu Ala Leu Asp Glu Met Leu Thr His Asp Ile Ala Lys Leu Met Pro	
380 385 390 395	
ctg ctg cgg cag gag gag ctg gag agc acc gag gtg ggc gtg cag ggg	1430
Leu Leu Arg Gln Glu Glu Leu Glu Ser Thr Glu Val Gly Val Gln Gly	
400 405 410	

ggc gct ttt gag ggc acc cac atg ggc ccg ttt gtg gag cgg gga cct	1478
Gly Ala Phe Glu Gly Thr His Met Gly Pro Phe Val Glu Arg Gly Pro	
415 420 425	
gac gag gcc atg gag gac ggc gag gag ggc tcg gac gac gag gcc gag	1526
Asp Glu Ala Met Glu Asp Gly Glu Glu Gly Ser Asp Asp Glu Ala Glu	
430 435 440	
tgg gtg gtg acc aaa gac aag tcc aaa tac gac gag atc ttc tac aac	1574
Trp Val Val Thr Lys Asp Lys Ser Lys Tyr Asp Glu Ile Phe Tyr Asn	
445 450 455	
ctg gcg cct gcc gac ggc aag ctg agc ggc tcc aag gcc aag acc tgg	1622
Leu Ala Pro Ala Asp Gly Lys Leu Ser Gly Ser Lys Ala Lys Thr Trp	
460 465 470 475	
atg gtg ggg acc aag ctc ccc aac tca gtg ctg ggg cgc atc tgg aag	1670
Met Val Gly Thr Lys Leu Pro Asn Ser Val Leu Gly Arg Ile Trp Lys	
480 485 490	
ctc agc gat gtg gac cgc gac ggc atg ctg gat gat gaa gag ttc gcg	1718
Leu Ser Asp Val Asp Arg Asp Gly Met Leu Asp Asp Glu Glu Phe Ala	
495 500 505	
ctg gcc agc cac ctc atc gag gcc aag ctg gaa ggc cac ggg ctg ccc	1766
Leu Ala Ser His Leu Ile Glu Ala Lys Leu Glu Gly His Gly Leu Pro	
510 515 520	
gcc aac ctg ccc cgt cgc ctg gtg cca ccc tcc aag cga cgc cac aag	1814
Ala Asn Leu Pro Arg Arg Leu Val Pro Pro Ser Lys Arg Arg His Lys	
525 530 535	
ggc tcc gcc gag tga gccggggcccc cctcccatgg ccctgctgtg gctccccagc	1869
Gly Ser Ala Glu *	
540	
tccagtcggc tgcacgcaca ccctgtctcc ggctcacaca cgccctgcct gccctccctg	1929
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cagcccccttc ccttgctcgg ggaaagcccc caattctgcc cacaccatt tatttccttc	2529

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cagctggtaa tctggactta aggattgctg ggccaccgcc tctctgccta ccaccattcc 3189
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ctgggattcc cagcccacc actgtcccc acccatggc tgggaggggc ctctgaacgg 3489
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ctgtccgctg ccaagggaaag tgacagccgc agccgggctc tcagccagcg gccgggcgcc 180
ccgcggacc   atg ctc tcc agt acg cag aac gcg ggc ggc tcc tat cag 228
              Met Leu Ser Ser Thr Gln Asn Ala Gly Gly Ser Tyr Gln
                1                   5                   10

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Arg Val Arg Gly Ala Leu Asp Thr Gln Lys Cys Ser Pro Glu Lys Ser	
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gcc tca ttt ttc agt aaa gtg aca tat tcc tgg ttt agc aga gta att	324
Ala Ser Phe Phe Ser Lys Val Thr Tyr Ser Trp Phe Ser Arg Val Ile	
30 35 40 45	
act tta ggc tat aag aga cct ttg gaa aga gag gat ctt ttt gaa cta	372
Thr Leu Gly Tyr Lys Arg Pro Leu Glu Arg Glu Asp Leu Phe Glu Leu	
50 55 60	
aag gaa agt gat tcc ttc tgc act gcg tgt ccc atc ttt gaa aaa caa	420
Lys Glu Ser Asp Ser Phe Cys Thr Ala Cys Pro Ile Phe Glu Lys Gln	
65 70 75	
tgg aga aag gaa gtt tta agg aat caa gag agg caa aaa gta aag gta	468
Trp Arg Lys Glu Val Leu Arg Asn Gln Glu Arg Gln Lys Val Lys Val	
80 85 90	
tct tgt tat aaa gag gca cat atc aag aaa cca tct cta ctc tat gca	516
Ser Cys Tyr Lys Glu Ala His Ile Lys Lys Pro Ser Leu Leu Tyr Ala	
95 100 105	
ttg tgg aac acc ttt aaa tcc atc ctg att caa gtt gcc tta ttc aaa	564
Leu Trp Asn Thr Phe Lys Ser Ile Leu Ile Gln Val Ala Leu Phe Lys	
110 115 120 125	
gtg ttt gct gat att ttg tcc ttc act agc cca ctc ata atg aag caa	612
Val Phe Ala Asp Ile Leu Ser Phe Thr Ser Pro Leu Ile Met Lys Gln	
130 135 140	
att atc att ttc tgt gaa cac agc tca gat ttt ggc tgg aat ggc tat	660
Ile Ile Ile Phe Cys Glu His Ser Ser Asp Phe Gly Trp Asn Gly Tyr	
145 150 155	
ggc tat gca gtg gca ctt ctt gtt gta gtc ttt ttg caa act ctg att	708
Gly Tyr Ala Val Ala Leu Leu Val Val Val Phe Leu Gln Thr Leu Ile	
160 165 170	
ctt cag caa tat caa cgt ttt aac atg ctc acc tca gca aaa gtt aag	756
Leu Gln Gln Tyr Gln Arg Phe Asn Met Leu Thr Ser Ala Lys Val Lys	
175 180 185	
aca gct gta aat gga ctg atc tac aaa aag gcc tta ctt tta tca aat	804
Thr Ala Val Asn Gly Leu Ile Tyr Lys Lys Ala Leu Leu Leu Ser Asn	
190 195 200 205	
gtt tct cga caa aag ttt tcc act ggg gaa att att aac ttg atg tca	852
Val Ser Arg Gln Lys Phe Ser Thr Gly Glu Ile Ile Asn Leu Met Ser	
210 215 220	
gca act cat gga ctt gac agc aaa cct caa tct cct ctg gtc tgc ccc	900
Ala Thr His Gly Leu Asp Ser Lys Pro Gln Ser Pro Leu Val Cys Pro	
225 230 235	

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ttt tca aat cct aat ggc cgt ata tct cct ttg gca aga gct ggg tcc      948
Phe Ser Asn Pro Asn Gly Arg Ile Ser Pro Leu Ala Arg Ala Gly Ser
      240                      245                      250

agc agt gtt agc agg ggt ggc agt cct tgt gtt tgt tat acc aat aaa      996
Ser Ser Val Ser Arg Gly Gly Ser Pro Cys Val Cys Tyr Thr Asn Lys
      255                      260                      265

tgc ttt agc tgc aac taa aataaa aaagttaaag gtaaaaaaat gactgcctca    1050
Cys Phe Ser Cys Asn *
      270                      275

tgttacatgt gtcaaacagg agctgagttt tctgacttga gttaacaatc accatctcgc    1110

taattatata gagagagtta caaatggaag tcatcgaatt ttatcattta cttattcact    1170

caaccagtat tgaacaagca tgtatcttat gtcagccagt gtttcaggca caggaagtac    1230

agcagtgagg ggaaatgaca agtccagctc tcatgagggg tagtggagga gacaggcatt    1290

aagcaagtac ataaatagag agaaaacatt tgtatatgaa aaagatttag taaaatacag    1350

tgatgaagag acaaaggatg ccattttaca tttaagatc                          1389

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<210> 232
<211> 707
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (56)..(439)

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<400> 232
ctactactac tactactaaa ttcgcggccg cgtcgaccat agcgctcacg caagc atg      58
                                         Met
                                         1

gtt aac gtc cct aaa acc cgc cgg act ttc tgt aag aag tgt ggc aag      106
Val Asn Val Pro Lys Thr Arg Arg Thr Phe Cys Lys Lys Cys Gly Lys
      5                      10                      15

cac caa ccc cat aaa gtg aca cag tac aag aag ggc aag gat tct ctg      154
His Gln Pro His Lys Val Thr Gln Tyr Lys Lys Gly Lys Asp Ser Leu
      20                      25                      30

tac gcc cag gga aag cgg cgt tat gac agg aag cag agt ggc tat ggt      202
Tyr Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser Gly Tyr Gly
      35                      40                      45

ggg caa act aag ccg att ttc cgg aaa aag gct aaa act aca aag aag      250
Gly Gln Thr Lys Pro Ile Phe Arg Lys Lys Ala Lys Thr Thr Lys Lys
      50                      55                      60                      65

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gtc aag tgt gct gca atc att ggt cac tcc ttc cat ata gat ttg ctg 307
Val Lys Cys Ala Ala Ile Ile Gly His Ser Phe His Ile Asp Leu Leu
55 60 65

cag cac ctc ctg cct ggc tgg gat aaa aat aag cta ctt cag gtc ttg 355
Gln His Leu Leu Pro Gly Trp Asp Lys Asn Lys Leu Leu Gln Val Leu
70 75 80 85

aga gct ctt gtg gat ata cat gtg ctc tgc tgg tct gac aag agc caa 403
Arg Ala Leu Val Asp Ile His Val Leu Cys Trp Ser Asp Lys Ser Gln
90 95 100

gag ctt cct gct gag ccc ata tta atg cct tcc tct atc gac atc att 451
Glu Leu Pro Ala Glu Pro Ile Leu Met Pro Ser Ser Ile Asp Ile Ile
105 110 115

gat gga acc aaa gag aag aag aca aag tta gat ggt ggg tca gcc tct 499
Asp Gly Thr Lys Glu Lys Lys Thr Lys Leu Asp Gly Gly Ser Ala Ser
120 125 130

ctt ctc agg cta caa gaa gaa tta tcc cta cca cag gca gca ctg aaa 547
Leu Leu Arg Leu Gln Glu Glu Leu Ser Leu Pro Gln Ala Ala Leu Lys
135 140 145

cag aca ata gac agc ttc cac ccc act aca cgc ctg cag caa cac agc 595
Gln Thr Ile Asp Ser Phe His Pro Thr Thr Arg Leu Gln Gln His Ser
150 155 160 165

ccg gct gca cag gct ctc gta tgc gac cat cat gct tgc agt agc ccg 643
Pro Ala Ala Gln Ala Leu Val Cys Asp His His Ala Cys Ser Ser Pro
170 175 180

gtc ttt gca cgg cta cct cta gag cac ctt cag aaa tgc cct taa gca 691
Val Phe Ala Arg Leu Pro Leu Glu His Leu Gln Lys Cys Pro *
185 190 195

tgctgggggtc acgtgtcatg caaaccttgg acagatgact gaacctctct atgccttgg 751

ttcttcatct gtgtagacgc cagtgcgat gtctccttcc tcaggtcggg gactatctgg 811

gaccaaggt tct 824

<210> 234
<211> 1077
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (239)..(946)

<400> 234
tttcgtctgg gccgcgcgc aggccttaca taggaagtcc ttctaaagag ctgcctgcc 60

gctgcccttc cccagatccc gaatatcctc ctggccaggt ggagcagaga acagttcctc 120

agctgggtcat gctgagctca taccctgatg gctgctccat gaggtcaaga ctgggtctcc 180

tccctcctcc cccttcacca atgcttggtc tcacggggct agttttgacc cccacgct 238
atg gca tca tgc acc tcc ctc cca gct cct ggc tct cgg cct aag aag 286
Met Ala Ser Ser Thr Ser Leu Pro Ala Pro Gly Ser Arg Pro Lys Lys
1 5 10 15

cct cta ggc aag atg gct gac tgg ttc agg cag acc ctg ctg aag aag 334
Pro Leu Gly Lys Met Ala Asp Trp Phe Arg Gln Thr Leu Leu Lys Lys
20 25 30

ccc aag aag agg ccc aac tcc cca gaa agc acc tcc agc gat gct tca 382
Pro Lys Lys Arg Pro Asn Ser Pro Glu Ser Thr Ser Ser Asp Ala Ser
35 40 45

cag cct acc tca cag gac agc cca cta ccc cca agc ctc agc tca gtc 430
Gln Pro Thr Ser Gln Asp Ser Pro Leu Pro Pro Ser Leu Ser Ser Val
50 55 60

acg tct ccc agc ctg cca ccc aca cat gcg agt gac agt ggc agt agt 478
Thr Ser Pro Ser Leu Pro Pro Thr His Ala Ser Asp Ser Gly Ser Ser
65 70 75 80

cgc tgg agc aaa gac tat gac gtc tgc gtg tgc cac agt gag gaa gac 526
Arg Trp Ser Lys Asp Tyr Asp Val Cys Val Cys His Ser Glu Glu Asp
85 90 95

ctg gtg gcc gcc cag gac ctg gtc tcc tac ttg gaa ggc agc act gcc 574
Leu Val Ala Ala Gln Asp Leu Val Ser Tyr Leu Glu Gly Ser Thr Ala
100 105 110

agc ctg cgc tgc ttc ctg caa ctc cgg gat gca acc cca ggc ggc gct 622
Ser Leu Arg Cys Phe Leu Gln Leu Arg Asp Ala Thr Pro Gly Gly Ala
115 120 125

ata gtg tcc gag ctg tgc cag gca ctg agc agt agt cac tgc cgg gtg 670
Ile Val Ser Glu Leu Cys Gln Ala Leu Ser Ser Ser His Cys Arg Val
130 135 140

ctg ctc atc acg ccg ggc ttc ctt cag gac ccc tgg tgc aag tac cag 718
Leu Leu Ile Thr Pro Gly Phe Leu Gln Asp Pro Trp Cys Lys Tyr Gln
145 150 155 160

atg ctg cag gcc ctg acc gag gct cca ggg gcc gag ggc tgc acc atc 766
Met Leu Gln Ala Leu Thr Glu Ala Pro Gly Ala Glu Gly Cys Thr Ile
165 170 175

ccc ctg ctg tgc ggc ctc agc aga gct gct tac cca cct gag ctc cga 814
Pro Leu Leu Ser Gly Leu Ser Arg Ala Ala Tyr Pro Pro Glu Leu Arg
180 185 190

ttc atg tac tac gtc gat ggc agg ggc cct gat ggt ggc ttt cgt caa 862
Phe Met Tyr Tyr Val Asp Gly Arg Gly Pro Asp Gly Gly Phe Arg Gln
195 200 205

gtc aaa gaa gct gtc atg cgt tgt aag cta cta cag gag gga gaa ggg 910
Val Lys Glu Ala Val Met Arg Cys Lys Leu Leu Gln Glu Gly Glu Gly
210 215 220

gaa cgg gat tca gct aca gta ttt gat cta ctt tga cttt taggagacag 960
Glu Arg Asp Ser Ala Thr Val Phe Asp Leu Leu *
225 230 235

ccctgtagcc tagtagttca aagcgcagct tctggaagag gctgtcgggg tttgtatcct 1020

ggctcctgcc cttattaacc cataaaaagt aacttggtca agttaaaaaa aaaaaaa 1077

<210> 235
<211> 916
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (169)..(738)

<400> 235
agctggctag cgtttaaact taagcttggt accgagctcg gatccactag tccagtgtgg 60

tggaattcca cagcccagta actttgctag tacctcttga gtgcaagggtg gagaattaag 120

atctggattt gagacggagc acggaacatt tcactcaggg gaagagct atg aac atg 177
Met Asn Met
1

ctg act gcc agc ctg ttg agg gca gtc ata gcc tcc atc tgt gtt gta 225
Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val Val
5 10 15

tcc agc atg gct cag aag gta act caa gcg cag act gaa att tct gtg 273
Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val
20 25 30 35

gtg gag aag gag gat gtg acc ttg gac tgt gtg tat gaa acc cgt gat 321
Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg Asp
40 45 50

act act tat tac tta ttc tgg tac aag caa cca cca agt gga gaa ttg 369
Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu
55 60 65

gtt ttc ctt att cgt cgg aac tct ttt gat gag caa aat gaa ata agt 417
Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser
70 75 80

ggg cgg tat tct tgg aac ttc cag aaa tcc acc agt tcc ttc aac ttc 465
Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe
85 90 95

acc atc aca gcc tca caa gtc gtg gac tca gca gta tac ttc tgt gct	513
Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala	
100 105 110 115	
ctg agt gag gcg gcc caa gaa acc agt ggc tct agg ttg acc ttt ggg	561
Leu Ser Glu Ala Ala Gln Glu Thr Ser Gly Ser Arg Leu Thr Phe Gly	
120 125 130	
gaa gga aca cag ctc aca gtg aat cct gat atc cag aac cct gac cct	609
Glu Gly Thr Gln Leu Thr Val Asn Pro Asp Ile Gln Asn Pro Asp Pro	
135 140 145	
gcc gtg tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc	657
Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys	
150 155 160	
cta ttc acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat	705
Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp	
165 170 175	
tct gat gtg tat atc aca gac aaa ctg tgc tag actgtgag gctagggatt	756
Ser Asp Val Tyr Ile Thr Asp Lys Leu Cys *	
180 185 190	
tcagaaccac cgggttgggc ctggagcaac aaatctgact ttgcatgggc aacgccttca	816
acaacaggct tatttcagaa gaacccttct tccccagccc caaaagggtcc cttgatggca	876
agctgccccga gaaagctttg aaacagatac caacctaaac	916

<210> 236
 <211> 876
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (38) .. (547)

<400> 236	
agtgtggtgg aattcgggag ccctgccccca ggggccc atg cag aat gcc acc aag	55
Met Gln Asn Ala Thr Lys	
1 5	
tat ggc aac atg aca gag gac cat gtg atg cac ctg ctc cag aat gct	103
Tyr Gly Asn Met Thr Glu Asp His Val Met His Leu Leu Gln Asn Ala	
10 15 20	
gac ccc ctg aag gtg tac ccg cca ctg aag ggg agc ttc ccg gag aac	151
Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly Ser Phe Pro Glu Asn	
25 30 35	
ctg aga cac ctt aag aac acc atg gag acc ata gac tgg aag gtc ttt	199
Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile Asp Trp Lys Val Phe	

40	45	50	
gag agc tgg atg cac cat tgg ctc ctg ttt gaa atg agc agg cac tcc			247
Glu Ser Trp Met His His Trp Leu Leu Phe Glu Met Ser Arg His Ser			
55	60	65	70
ttg gag caa aag ccc act gac gct cca ccg aaa gta ctg acc aag tgc			295
Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys Val Leu Thr Lys Cys			
	75	80	85
cag gaa gag gtc agc cac atc cct gct gtc cac ccg ggt tca ttc agg			343
Gln Glu Glu Val Ser His Ile Pro Ala Val His Pro Gly Ser Phe Arg			
	90	95	100
ccc aag tgc gac gag aac ggc aac tat ctg cca ctc cag tgc tat ggg			391
Pro Lys Cys Asp Glu Asn Gly Asn Tyr Leu Pro Leu Gln Cys Tyr Gly			
	105	110	115
agc atc ggc tac tgc tgg tgt gtc ttc ccc aac ggc acg gag gtc ccc			439
Ser Ile Gly Tyr Cys Trp Cys Val Phe Pro Asn Gly Thr Glu Val Pro			
	120	125	130
aac acc aga agc cgc ggg cac cat aac tgc agt gag tca ctg gaa ctg			487
Asn Thr Arg Ser Arg Gly His His Asn Cys Ser Glu Ser Leu Glu Leu			
	135	140	145
gag gac ccg tct tct ggg ctg ggt gtg acc aag cag gat ctg ggc cca			535
Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys Gln Asp Leu Gly Pro			
	155	160	165
gtc ccc atg tga gag cagcagaggc ggtcttcaac atcctgccag cccacacag			590
Val Pro Met *			
	170		
ctacagcttt cttgctccct tcagcccca gccctcccc catctccac cctgtacctc			650
atcccatgag accctggtgc ctggctcttt cgtcaccctt ggacaagaca aaccaagtgc			710
gaacagcaga taacaatgca gcaaggccct gctgccaat ctccatctgt caacaggggc			770
ggtcgacgcg gccgcgaatt cggatcctcg agagatctct ttttttgggt ttggtggggt			830
gtcttcatca tcggatatac taggtatata catcggccta tcaagg			876

<210> 237
 <211> 753
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (168)..(419)

 <400> 237

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gtccgtgctc accgcccggc gtccaggtga gtctcccatc tgcagagacg cggacgcgcc      60
ggcccgagct tggcctgcgg agcgcggtgg acggtttggc gccaccagg cgatcaatac      120
tttggaatttt taatttctag atttggcaat tcttcgctga agtcacatc  atg agc ttt      176
                                     Met Ser Phe
                                     1

ttc caa ctc ctg atg aaa agg aag gaa ctc att ccc ttg gtg gtg ttc      224
Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu Val Val Phe
      5              10              15

atg act gtg gcg gcg ggt gga gcc tca tct ttc gct gtg tat tct ctt      272
Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val Tyr Ser Leu
      20              25              30              35

tgg aaa acc gat gtg atc ctt gat cga aaa aaa aat cca gaa cct tgg      320
Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro Glu Pro Trp
              40              45              50

gaa act gtg gac cct act gta cct caa aag ctt ata aca atc aac caa      368
Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr Ile Asn Gln
              55              60              65

caa tgg aaa ccc att gaa gag ttg caa aat gtc caa agg gtg acc aaa      416
Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg Val Thr Lys
              70              75              80

tga cgag ccctcgctc tttcttctga agagtactct ataaatctag tggaaacatt      473
*

tctgcacaaa ctagattctg gacaccagtg tgcggaaatg cttctgctac attttttaggg      533
tttgtctaca ttttttgggc tctggataag gaattaaagg agtgcagcaa taactgcact      593
gtctaaaagt ttgtgcttat tttcttgtaa atttgaatat tgcattattga aatttttgtt      653
tatgatctat gaatgttttt cttaaaattt acaaagcttt gtaaattaga ttttctttaa      713
taaaatgccca tttgtgcaag atttctcaaa aaaaaaaaaa      753

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<210> 238
 <211> 1395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50) .. (1060)

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<400> 238
gagtgggtgga attccgctgg cctcgctcgg tgcgcgcctc cctccccgc      atg cag      55
                                     Met Gln

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ccc gcc gag cgc tcg cgg gtc ccc agg atc gac ccg tac gga ttc gag	103
Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly Phe Glu	
5 10 15	
cgg cct gag gac ttc gac gac gcc gcc tac gag aag ttt ttc tcc agc	151
Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe Ser Ser	
20 25 30	
tac ctg gtc acg ctc acc cgc agg gcg atc aaa tgg tcc cgg ctg ctg	199
Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg Leu Leu	
35 40 45 50	
cag ggc ggg ggc gtc ccc agg agc cgg aca gtg aag cgc tat gtc cgg	247
Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr Val Arg	
55 60 65	
aaa ggg gtc ccg ctg gag cac cgt gcc cgc gtc tgg atg gtg ctg agt	295
Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val Leu Ser	
70 75 80	
ggg gcc cag gcg cag atg gac cag aat ccc ggc tac tac cac cag ctt	343
Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His Gln Leu	
85 90 95	
ctc cag gga gag aga aac ccc agg ctg gag gac gcc atc agg aca gac	391
Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg Thr Asp	
100 105 110	
ctg aac cgg acc ttc ccc gac aac gtg aag ttc cgg aag acc acg gac	439
Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr Thr Asp	
115 120 125 130	
ccc tgc tta cag agg acc ctg tac aat gtg ctg ctg gca tat ggg cac	487
Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr Gly His	
135 140 145	
cat aac cag gga gtg ggc tac tgc cag gga atg aat ttt ata gca gga	535
His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile Ala Gly	
150 155 160	
tat ctg att ctt ata aca aat aat gaa gaa gaa tct ttt tgg ctg tta	583
Tyr Leu Ile Leu Ile Thr Asn Asn Glu Glu Glu Ser Phe Trp Leu Leu	
165 170 175	
gat gct ctt gtt gga aga ata cta cca gat tac tac agc ccg gcc atg	631
Asp Ala Leu Val Gly Arg Ile Leu Pro Asp Tyr Tyr Ser Pro Ala Met	
180 185 190	
ctg ggc ctg aag acc gac cag gag gtc ctc ggg gag ctg gtg cgg gcg	679
Leu Gly Leu Lys Thr Asp Gln Glu Val Leu Gly Glu Leu Val Arg Ala	
195 200 205 210	
aag ctg ccg gct gtg ggg gcc ctg atg gag cgt ctc ggt gtg ctg tgg	727
Lys Leu Pro Ala Val Gly Ala Leu Met Glu Arg Leu Gly Val Leu Trp	
215 220 225	

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acg ctg ctg gtg tcc cgc tgg ttc atc tgc ctg ttt gtg gac atc ttg      775
Thr Leu Leu Val Ser Arg Trp Phe Ile Cys Leu Phe Val Asp Ile Leu
      230                      235                      240

ccc gtg gag aca gtg ctt cgg atc tgg gac tgt ttg ttt aac gaa ggc      823
Pro Val Glu Thr Val Leu Arg Ile Trp Asp Cys Leu Phe Asn Glu Gly
      245                      250                      255

tcg aag att atc ttc cgg gtg gcc ctg acc tta att aag cag cac cag      871
Ser Lys Ile Ile Phe Arg Val Ala Leu Thr Leu Ile Lys Gln His Gln
      260                      265                      270

gag ttg att ttg gaa gcc acc agc gtt cca gac att tgc gat aag ttt      919
Glu Leu Ile Leu Glu Ala Thr Ser Val Pro Asp Ile Cys Asp Lys Phe
      275                      280                      285                      290

aag cag ata acc aaa ggg agt ttc gtg atg gag tgt cac acg ttt atg      967
Lys Gln Ile Thr Lys Gly Ser Phe Val Met Glu Cys His Thr Phe Met
      295                      300                      305

cag aaa ata ttt tca gaa cct gga agc tta tcc atg gcc acc gtc gcc      1015
Gln Lys Ile Phe Ser Glu Pro Gly Ser Leu Ser Met Ala Thr Val Ala
      310                      315                      320

aag ctc cgc gag agc tgc agg gcc cgg ctg ctg gca cag ggg tga gcg      1063
Lys Leu Arg Glu Ser Cys Arg Ala Arg Leu Leu Ala Gln Gly *
      325                      330                      335

tgctgtccc ctgcgttgct cgtctctaca ctgacgatgc ccctttccag agttgacact      1123

ggaccaactt tcaactgttt ccttttttagt gttgtaaata cttgacatca ctacacttta      1183

gttgtgaatt ttttaaaaga gcagtttaaa atcagggtcat tctaccagct tttgatgatt      1243

agctatgaag tcatactttt taaagaaaac ttattttttac ctgagagatc aataatatat      1303

aaaatgtgag tgtggggttg tatctaataa agtatgccaa cacctgtggt tgtgatcagt      1363

ttctcagctg actggaaatt aaaaaaaaaa aa                                  1395

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<210> 239
<211> 767
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (78)..(326)

<220>
<221> misc_feature
<222> (1)...(767)
<223> n = a,t,c or g

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<400> 239
 ccggtccgga attcccggtt cgacccacgc gtccgccctt ctctcttctt tgggtgcttct 60
 ttttctgct cggcattc atg gct gcc ctc aga tcc ctt gtg aag ccc aag 110
 Met Ala Ala Leu Arg Ser Leu Val Lys Pro Lys
 1 5 10
 atc gtc aaa aag aga acc aag aaa ttc atc cgg cac cag tca gac cga 158
 Ile Val Lys Lys Arg Thr Lys Lys Phe Ile Arg His Gln Ser Asp Arg
 15 20 25
 tat gtc aaa atc aag atg aga aga ata atg tct ggg gtg aag gtg aag 206
 Tyr Val Lys Ile Lys Met Arg Arg Ile Met Ser Gly Val Lys Val Lys
 30 35 40
 cac cca gcc caa gac tca gca gcc agg aag tgg ccc agc gct ctt tat 254
 His Pro Ala Gln Asp Ser Ala Ala Arg Lys Trp Pro Ser Ala Leu Tyr
 45 50 55
 acc acg ggt gca gga att cac aca gaa aag tgg agg cca agg cgt gag 302
 Thr Thr Gly Ala Gly Ile His Thr Glu Lys Trp Arg Pro Arg Arg Glu
 60 65 70 75
 aat tcc tca atg act gcc ctc taa aggaagagat ccaaagaaat cctgaggaag 356
 Asn Ser Ser Met Thr Ala Leu *
 80
 cacaacaaac aaaaacactc tggatcagaa cttcctgtgc cagcgttaca tcagggtttt 416
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gaaaagcttg cagaatttct tctgaaatta cttaaaatta ctgtatgcat aaacttacaa 180

aaacat atg cta tac caa ggc aga gaa aag aaa aaa agt gaa gtg gct 228
Met Leu Tyr Gln Gly Arg Glu Lys Lys Lys Ser Glu Val Ala
1 5 10

aca aag gtc cct ggg gca tca cct gct cac cta gga acc agg agt act 276
Thr Lys Val Pro Gly Ala Ser Pro Ala His Leu Gly Thr Arg Ser Thr
15 20 25 30

gga tac tgt tcc gtt act ggt aac cta tct gga tgt aaa ggt tca taa 324
Gly Tyr Cys Ser Val Thr Gly Asn Leu Ser Gly Cys Lys Gly Ser *
35 40 45

gttacaatgc tttttttgtt taataaaaaa aaaaagtctg tacttttaca gccaaaagtg 384

aaaatgccac acatcctctt tacgctttca tgtacactaa gtcactccat ttggttgata 444

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1 5

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Glu Glu Asp His Ala Glu Glu Pro Ser Lys Asp Gly Gly Ala Leu Glu
10 15 20 25

gag aag gat tcg gac ggg gca gcc tcc aag gag gac agc ggc ccc agc 149
Glu Lys Asp Ser Asp Gly Ala Ala Ser Lys Glu Asp Ser Gly Pro Ser
30 35 40

acc agg cag gct tca gga gag gcc tcc tcg ctg cgg gac tac gcg gcc 197
Thr Arg Gln Ala Ser Gly Glu Ala Ser Ser Leu Arg Asp Tyr Ala Ala
45 50 55

tcc acc atg acc gag ttc ctc ggc atg ttt ggc tat gat gac cag aac 245
Ser Thr Met Thr Glu Phe Leu Gly Met Phe Gly Tyr Asp Asp Gln Asn
60 65 70

acg cgg gac gag ctg gcc agg aag atc agc ttt gag aag ctg cac gcg	293
Thr Arg Asp Glu Leu Ala Arg Lys Ile Ser Phe Glu Lys Leu His Ala	
75 80 85	
ggc tcc acc ccg gag gca gcc acc tcc tcc atg ctg ccc acc tcc gag	341
Gly Ser Thr Pro Glu Ala Ala Thr Ser Ser Met Leu Pro Thr Ser Glu	
90 95 100 105	
gat acc ctc agc aag cgg gcg cgg ttc tct aag tat gag gag tac atc	389
Asp Thr Leu Ser Lys Arg Ala Arg Phe Ser Lys Tyr Glu Glu Tyr Ile	
110 115 120	
cgc aag ctc aag gct ggc gag cag ctc tcc tgg ccg gcc ccc agc acc	437
Arg Lys Leu Lys Ala Gly Glu Gln Leu Ser Trp Pro Ala Pro Ser Thr	
125 130 135	
aag acc gag gag cgg gtg ggc aag gag gtg gtg ggc acc ctg ccc ggc	485
Lys Thr Glu Glu Arg Val Gly Lys Glu Val Val Gly Thr Leu Pro Gly	
140 145 150	
ctg cgg ctg ccc agc agc acg gcc cac ctg gag acc aag gcc acc atc	533
Leu Arg Leu Pro Ser Ser Thr Ala His Leu Glu Thr Lys Ala Thr Ile	
155 160 165	
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Leu Pro Leu Pro Ser His Ser Ser Val Gln Met Gln Asn Leu Val Ala	
170 175 180 185	
cgg gcc tcc aag tac gac ttc ttc atc caa aaa ctg aag acc ggc gag	629
Arg Ala Ser Lys Tyr Asp Phe Phe Ile Gln Lys Leu Lys Thr Gly Glu	
190 195 200	
aat ctg cgg ccc cag aac ggg agc acc tac aag aag cca tcc aag tac	677
Asn Leu Arg Pro Gln Asn Gly Ser Thr Tyr Lys Lys Pro Ser Lys Tyr	
205 210 215	
gac ctg gag aat gtc aag tac ctg cac ctc ttc aaa ccc ggg gag ggc	725
Asp Leu Glu Asn Val Lys Tyr Leu His Leu Phe Lys Pro Gly Glu Gly	
220 225 230	
agc ccc gac atg ggc ggg gcc atc gcc ttc aag aca ggc aag gtg ggc	773
Ser Pro Asp Met Gly Gly Ala Ile Ala Phe Lys Thr Gly Lys Val Gly	
235 240 245	
cgc cct tcc aag tac gac gtc cgg ggc atc cag aag cca ggc ccc gcc	821
Arg Pro Ser Lys Tyr Asp Val Arg Gly Ile Gln Lys Pro Gly Pro Ala	
250 255 260 265	
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Lys Val Pro Pro Thr Pro Ser Leu Ala Pro Ala Pro Leu Ala Ser Val	
270 275 280	
ccc agt gcc ccc aac gcc ccc ggg cca ggg cca gag cct cct gcc tcc	917
Pro Ser Ala Pro Asn Ala Pro Gly Pro Gly Pro Glu Pro Pro Ala Ser	
285 290 295	
ctg tcc ttc aac act ccc gag tac ctg aag tca acc ttc tcc aaa aca	965

Leu Ser Phe Asn Thr Pro Glu Tyr Leu Lys Ser Thr Phe Ser Lys Thr	
300 305 310	
gac tcc atc acc acg ggg acc gtc tcc act gtc aag aac gga ctg ccc	1013
Asp Ser Ile Thr Thr Gly Thr Val Ser Thr Val Lys Asn Gly Leu Pro	
315 320 325	
aca gat aaa cca gcc gtc act gaa gat gta aac att tac cag aaa tat	1061
Thr Asp Lys Pro Ala Val Thr Glu Asp Val Asn Ile Tyr Gln Lys Tyr	
330 335 340 345	
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Ile Ala Arg Phe Ser Gly Ser Gln His Cys Gly His Ile His Cys Ala	
350 355 360	
tac cag tac cgc gag cac tac cac tgc ctt gac cct gag tgt aac tac	1157
Tyr Gln Tyr Arg Glu His Tyr His Cys Leu Asp Pro Glu Cys Asn Tyr	
365 370 375	
cag agg ttc acg agt aag cag gac gtg atc cgc cac tac aac atg cac	1205
Gln Arg Phe Thr Ser Lys Gln Asp Val Ile Arg His Tyr Asn Met His	
380 385 390	
aag aag cgc gac aac tcc ctg cag cac ggc ttc atg cgt ttc agc ccg	1253
Lys Lys Arg Asp Asn Ser Leu Gln His Gly Phe Met Arg Phe Ser Pro	
395 400 405	
ctg gac gac tgc agc gtc tac tac cac ggc tgc cac ctc aat ggg aag	1301
Leu Asp Asp Cys Ser Val Tyr Tyr His Gly Cys His Leu Asn Gly Lys	
410 415 420 425	
agc acc cac tat cac tgc atg cag gtg ggc tgt aac aag gtg tac acg	1349
Ser Thr His Tyr His Cys Met Gln Val Gly Cys Asn Lys Val Tyr Thr	
430 435 440	
agc acg tct gac gtg atg acc cac gag aac ttc cac aag aag aat acc	1397
Ser Thr Ser Asp Val Met Thr His Glu Asn Phe His Lys Lys Asn Thr	
445 450 455	
cag ctc att aac gac ggc ttc cag cgc ttc cga gcc acc gaa gac tgt	1445
Gln Leu Ile Asn Asp Gly Phe Gln Arg Phe Arg Ala Thr Glu Asp Cys	
460 465 470	
ggc aca gcc gac tgc cag ttc tac gga cag aag acc acg cac ttc cac	1493
Gly Thr Ala Asp Cys Gln Phe Tyr Gly Gln Lys Thr Thr His Phe His	
475 480 485	
tgc agg cgc ccc ggc tgc aca ttc act ttc aag aac aag tgt gac atc	1541
Cys Arg Arg Pro Gly Cys Thr Phe Thr Phe Lys Asn Lys Cys Asp Ile	
490 495 500 505	
gag aag cac aag agc tac cac atc aag gac gat gcc tac gcc aag gac	1589
Glu Lys His Lys Ser Tyr His Ile Lys Asp Asp Ala Tyr Ala Lys Asp	
510 515 520	
ggc ttc aag aag ttc tac aag tac gag gag tgc aag tac gag ggc tgc	1637
Gly Phe Lys Lys Phe Tyr Lys Tyr Glu Glu Cys Lys Tyr Glu Gly Cys	

525	530	535	
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Val Tyr Ser Lys Ala Thr Asn His Phe His Cys Ile Arg Ala Gly Cys			
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ggc ttc acc ttc acc tcc acc agc cag atg acc tct cac aag cgc aag			1733
Gly Phe Thr Phe Thr Ser Thr Ser Gln Met Thr Ser His Lys Arg Lys			
555	560	565	
cat gag cgc cgg cac atc cgc tcc tcg ggc gcg ctg ggg ctg ccg ccc			1781
His Glu Arg Arg His Ile Arg Ser Ser Gly Ala Leu Gly Leu Pro Pro			
570	575	580	585
tcg ctg ctg ggc gcc aag gac acg gag cac gag gag tcc agc aac gac			1829
Ser Leu Leu Gly Ala Lys Asp Thr Glu His Glu Glu Ser Ser Asn Asp			
590	595	600	
gac ctt gtt gac ttc tcc gcc ctg agc agc aag aac tcc agc ctg agc			1877
Asp Leu Val Asp Phe Ser Ala Leu Ser Ser Lys Asn Ser Ser Leu Ser			
605	610	615	
gcc tcc cct acc agc cag cag tcc tct gcg tcc ctg gct gcc gcc act			1925
Ala Ser Pro Thr Ser Gln Gln Ser Ser Ala Ser Leu Ala Ala Ala Thr			
620	625	630	
gcc gcc acc gag gct ggg ccc agt gcc acc aaa cct ccc aac agc aag			1973
Ala Ala Thr Glu Ala Gly Pro Ser Ala Thr Lys Pro Pro Asn Ser Lys			
635	640	645	
atc tcg ggg ctg ctg ccc cag ggc ctg cct ggc tcg atc ccc ctg gcc			2021
Ile Ser Gly Leu Leu Pro Gln Gly Leu Pro Gly Ser Ile Pro Leu Ala			
650	655	660	665
ctg gcc ctc tcc aac tcg ggc ctg ccc acc ccc acg ccc tac ttc ccc			2069
Leu Ala Leu Ser Asn Ser Gly Leu Pro Thr Pro Thr Pro Tyr Phe Pro			
670	675	680	
ata ctg gct ggc cgt ggg agc acc tcc ctg cct gtg ggc acc ccc agc			2117
Ile Leu Ala Gly Arg Gly Ser Thr Ser Leu Pro Val Gly Thr Pro Ser			
685	690	695	
ctc ctg ggt gcc gtg tcg tct ggg tca gca gcc tca gcc acc cct gac			2165
Leu Leu Gly Ala Val Ser Ser Gly Ser Ala Ala Ser Ala Thr Pro Asp			
700	705	710	
aca ccc acg ctg gtc gcc tcg gga gct gga gac tca gcc ccc gtg gct			2213
Thr Pro Thr Leu Val Ala Ser Gly Ala Gly Asp Ser Ala Pro Val Ala			
715	720	725	
gcc gcc tct gtc ccg gca cca ccc gcc tcc atc atg gag agg atc tct			2261
Ala Ala Ser Val Pro Ala Pro Pro Ala Ser Ile Met Glu Arg Ile Ser			
730	735	740	745
gca agc aag ggc ctc atc tcg ccc atg atg gcc agg ctg gct gca gct			2309
Ala Ser Lys Gly Leu Ile Ser Pro Met Met Ala Arg Leu Ala Ala Ala			
750	755	760	

gcc ctc aag ccc tct gcc acc ttt gac cca gga agc ggg cag cag gtc Ala Leu Lys Pro Ser Ala Thr Phe Asp Pro Gly Ser Gly Gln Gln Val 765 770 775	2357
acc cca gcc agg ttc ccc ccg gcc caa gtg aag ccg gaa ccc ggt gag Thr Pro Ala Arg Phe Pro Pro Ala Gln Val Lys Pro Glu Pro Gly Glu 780 785 790	2405
agc acc ggc gcc cca ggc ccc cac gaa gcc tcc cag gac cgc agt cta Ser Thr Gly Ala Pro Gly Pro His Glu Ala Ser Gln Asp Arg Ser Leu 795 800 805	2453
gac ctg act gtg aag gag ccc agc aac gaa tca aat ggc cac gca gtc Asp Leu Thr Val Lys Glu Pro Ser Asn Glu Ser Asn Gly His Ala Val 810 815 820 825	2501
ccg gca aat tca tct ctt tta tcc tcg ctt atg aat aag atg tct cag Pro Ala Asn Ser Ser Leu Leu Ser Ser Leu Met Asn Lys Met Ser Gln 830 835 840	2549
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ggg agc ccc gct gcg gag ccc tcg ccc ttc cta ggc aag gcc gtg aag Gly Ser Pro Ala Ala Glu Pro Ser Pro Phe Leu Gly Lys Ala Val Lys 860 865 870	2645
gcg ctg gtt cag gag aag ttg gca gag ccc tgg aag gtg tac ctg cgc Ala Leu Val Gln Glu Lys Leu Ala Glu Pro Trp Lys Val Tyr Leu Arg 875 880 885	2693
agg ttt ggt aca aag gac ttc tgt gac ggc cag tgt gac ttc ctc cac Arg Phe Gly Thr Lys Asp Phe Cys Asp Gly Gln Cys Asp Phe Leu His 890 895 900 905	2741
aag gcc cac ttc cac tgc gtg gtg gag gaa tgc ggc gcg ctc ttc agc Lys Ala His Phe His Cys Val Val Glu Glu Cys Gly Ala Leu Phe Ser 910 915 920	2789
acc ttg gac ggg gcc atc aag cac gca aac ttc cac ttc cgg aca gag Thr Leu Asp Gly Ala Ile Lys His Ala Asn Phe His Phe Arg Thr Glu 925 930 935	2837
gga gga gca gca aaa gga aac aca gag gct gcc ttt ccg gcc tcg gcc Gly Gly Ala Ala Lys Gly Asn Thr Glu Ala Ala Phe Pro Ala Ser Ala 940 945 950	2885
gcc gag acc aaa cct ccc atg gcc ccc tcg tcc cct ccg gtc cct cct Ala Glu Thr Lys Pro Pro Met Ala Pro Ser Ser Pro Pro Val Pro Pro 955 960 965	2933
gtc acc acg gcc acg gtg tcc tct ctg gag ggg ccc gct ccc agc ccg Val Thr Thr Ala Thr Val Ser Ser Leu Glu Gly Pro Ala Pro Ser Pro 970 975 980 985	2981

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gcc tcc gtg ccc tcc acc ccc acc ctg ctc gcc tgg aag cag ctg gct      3029
Ala Ser Val Pro Ser Thr Pro Thr Leu Leu Ala Trp Lys Gln Leu Ala
          990                      995                      1000

tcc acc ata ccc cag atg cct cag atc cca gcg tca gtg cct cac ctg      3077
Ser Thr Ile Pro Gln Met Pro Gln Ile Pro Ala Ser Val Pro His Leu
          1005                      1010                      1015

ccc gcc tcg ccc ttg gca acg act tct cta gag aac gcc aag ccc cag      3125
Pro Ala Ser Pro Leu Ala Thr Thr Ser Leu Glu Asn Ala Lys Pro Gln
          1020                      1025                      1030

gtc aaa ccc gga ttc ctc cag ttc cag gag aag tga gtcc ctcatgagc      3175
Val Lys Pro Gly Phe Leu Gln Phe Gln Glu Lys *
          1035                      1040                      1045

cgggagtgccc gcgttcccct cgcgtctcgg gagtaggtgc tagcaagggc gctaggaggc      3235

cctgttccctc actgcggatg gtgctgctgt cccagcctc tctggggcat ggccatcggg      3295

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cagcccgcgt gggccgatgg tggcggcagt ggctactgct cctgcagggc atgtggtgat      3415

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aaagctttta gagttctgat gcctatttaa gtaaattaac tcttttcccc ccaaattct      180

taggcttgaa g atg cag tgg acg cca gag cat gcc cag tgg cca gaa cag      230
          Met Gln Trp Thr Pro Glu His Ala Gln Trp Pro Glu Gln

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His Phe Asp Ile Thr Ser Thr Thr Arg Ser Pro Ala His Lys Val Glu			
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gcc tac aga ggt cat ctg cag cgc acc tat cag tac gcc tgg gcg aat			326
Ala Tyr Arg Gly His Leu Gln Arg Thr Tyr Gln Tyr Ala Trp Ala Asn			
30	35	40	45
gat gac ata tct gct ctg act gca tcc aac cta cta aaa aaa tat gca			374
Asp Asp Ile Ser Ala Leu Thr Ala Ser Asn Leu Leu Lys Lys Tyr Ala			
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gag aag tat tcc ggc att ttg gaa ggt cct gtg gac cga ccc gta ctc			422
Glu Lys Tyr Ser Gly Ile Leu Glu Gly Pro Val Asp Arg Pro Val Leu			
65	70	75	
agc aac tat tcg gac aca cca tca gga cta gtg aac ggt cgg aaa aat			470
Ser Asn Tyr Ser Asp Thr Pro Ser Gly Leu Val Asn Gly Arg Lys Asn			
80	85	90	
gaa agt gaa ccc tgg cag cct tcc ttg aat tca gaa gct gtt tat ccc			518
Glu Ser Glu Pro Trp Gln Pro Ser Leu Asn Ser Glu Ala Val Tyr Pro			
95	100	105	
atg aac tgt gtt ccg gat gtt atc act gcc agc aaa gct gga gtc agt			566
Met Asn Cys Val Pro Asp Val Ile Thr Ala Ser Lys Ala Gly Val Ser			
110	115	120	125
tca gcc ctc cct cca gca gat gtc tct gcg agt ata gga agc tct cct			614
Ser Ala Leu Pro Pro Ala Asp Val Ser Ala Ser Ile Gly Ser Ser Pro			
130	135	140	
ggg gta gcc agc aac ctg aca gaa cct agt tat tca agt agt acc tgt			662
Gly Val Ala Ser Asn Leu Thr Glu Pro Ser Tyr Ser Ser Ser Thr Cys			
145	150	155	
gga agc cac act gta ccc agt ctt cat gca ggg ctc cca tct cag gaa			710
Gly Ser His Thr Val Pro Ser Leu His Ala Gly Leu Pro Ser Gln Glu			
160	165	170	
tat gcc cca gga tac aac gga tca tat ttg cat tct act tat agt agc			758
Tyr Ala Pro Gly Tyr Asn Gly Ser Tyr Leu His Ser Thr Tyr Ser Ser			
175	180	185	
cag cca gca cct gca ctt cct tca cct cat ccg tct cct ttg cat agc			806
Gln Pro Ala Pro Ala Leu Pro Ser Pro His Pro Ser Pro Leu His Ser			
190	195	200	205
tct ggg cta cta cag ccc cca cca cca cct cct ccg cca cca gcc ttg			854
Ser Gly Leu Leu Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Leu			
210	215	220	
gtc cca ggc tac aat ggg act tct aac ctc tcc agt tac agc tat ccg			902
Val Pro Gly Tyr Asn Gly Thr Ser Asn Leu Ser Ser Tyr Ser Tyr Pro			
225	230	235	

tct gct agc tat cct cct cag act gct gtg ggg tct ggg tac agc cct	950
Ser Ala Ser Tyr Pro Pro Gln Thr Ala Val Gly Ser Gly Tyr Ser Pro	
240 245 250	
ggg ggg gca ccg cct ccg cct tca gcg tac ctg cct tca gga att cct	998
Gly Gly Ala Pro Pro Pro Pro Ser Ala Tyr Leu Pro Ser Gly Ile Pro	
255 260 265	
gct ccc acc ccc cta ccc ccc acc act gtt cct ggc tac acc tac cag	1046
Ala Pro Thr Pro Leu Pro Pro Thr Thr Val Pro Gly Tyr Thr Tyr Gln	
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Gly His Gly Leu Thr Pro Ile Ala Pro Ser Ala Leu Thr Asn Ser Ser	
290 295 300	
gca agt tct ctc aaa agg aaa gct ttc tac atg gca ggg caa gga gat	1142
Ala Ser Ser Leu Lys Arg Lys Ala Phe Tyr Met Ala Gly Gln Gly Asp	
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atg gac tcc agt tat gga aat tac agc tat ggc caa cag aga tct aca	1190
Met Asp Ser Ser Tyr Gly Asn Tyr Ser Tyr Gly Gln Gln Arg Ser Thr	
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cag agt cct atg tac aga atg ccc gac aac agc att tca aac aca aat	1238
Gln Ser Pro Met Tyr Arg Met Pro Asp Asn Ser Ile Ser Asn Thr Asn	
335 340 345	
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Arg Gly Asn Gly Phe Asp Arg Ser Ala Glu Thr Ser Ser Leu Ala Phe	
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aag cca acg aag cag cta atg tcc tct gaa cag caa agg aaa ttc agc	1334
Lys Pro Thr Lys Gln Leu Met Ser Ser Glu Gln Gln Arg Lys Phe Ser	
370 375 380	
agc cag tcc agt agg gct ctg acc cct cct tcc tac agt act gct aaa	1382
Ser Gln Ser Ser Arg Ala Leu Thr Pro Pro Ser Tyr Ser Thr Ala Lys	
385 390 395	
aat tca ttg gga tca aga tcc agt gaa tcc ttt ggg aag tac aca tcg	1430
Asn Ser Leu Gly Ser Arg Ser Ser Glu Ser Phe Gly Lys Tyr Thr Ser	
400 405 410	
cca gta atg agt gag cat ggg gac gag cac agg cag ctc ctc tct cac	1478
Pro Val Met Ser Glu His Gly Asp Glu His Arg Gln Leu Leu Ser His	
415 420 425	
cca atg caa ggc cct gga ctc cgt gca gct acc tca tcc aac cac tct	1526
Pro Met Gln Gly Pro Gly Leu Arg Ala Ala Thr Ser Ser Asn His Ser	
430 435 440 445	
gtg gac gag caa ctg aag aat act gac acg cac ctc atc gac ctg gta	1574
Val Asp Glu Gln Leu Lys Asn Thr Asp Thr His Leu Ile Asp Leu Val	
450 455 460	

acc aat gag att atc acc caa gga cct cca gtg gac tgg aat gac att	1622
Thr Asn Glu Ile Ile Thr Gln Gly Pro Pro Val Asp Trp Asn Asp Ile	
465 470 475	
gct ggt ctc gac ctg gtg aag gct gtc att aaa gag gag gtt tta tgg	1670
Ala Gly Leu Asp Leu Val Lys Ala Val Ile Lys Glu Glu Val Leu Trp	
480 485 490	
cca gtg ttg agg tca gac gcg ttc agt gga ctg acg gcc tta cct cgg	1718
Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr Ala Leu Pro Arg	
495 500 505	
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Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys Thr Leu Leu Gly	
510 515 520 525	
aga tgc atc gct agt cag ctg ggg gcc aca ttt ttc aaa att gcc ggt	1814
Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe Lys Ile Ala Gly	
530 535 540	
tct gga cta gtc gcc aag tgg tta gga gaa gca gag aaa att atc cat	1862
Ser Gly Leu Val Ala Lys Trp Leu Gly Glu Ala Glu Lys Ile Ile His	
545 550 555	
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Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser Val Ile Phe Val	
560 565 570	
agt gac att gac atg ctt ctc tcc tct caa gtg aat gag gaa cat agt	1958
Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn Glu Glu His Ser	
575 580 585	
cca gtc agt cgg atg aga acc gaa ttt ctg atg caa ctg gac act gta	2006
Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln Leu Asp Thr Val	
590 595 600 605	
cta act tcg gct gag gac caa atc gta gta att tgt gcc acc agt aaa	2054
Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys Ala Thr Ser Lys	
610 615 620	
cca gaa gaa ata gat gaa tcc ctt cgg agg tac ttc atg aaa cga ctt	2102
Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe Met Lys Arg Leu	
625 630 635	
tta atc cca ctt cct gac agc aca gcg agg cac cag ata ata gta caa	2150
Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln Ile Ile Val Gln	
640 645 650	
ctg ctc tca cag cac aat tac tgt ctc aat gac aag gag ttt gca ctg	2198
Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys Glu Phe Ala Leu	
655 660 665	
ctc gtc cag cgc aca gaa ggc ttt tct gga cta gat gtg gct cat ttg	2246
Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp Val Ala His Leu	
670 675 680 685	
tgt cag gaa gca gtg gtg ggc ccc ctc cat gcc atg cca gcc aca gac	2294

Cys	Gln	Glu	Ala	Val	Val	Gly	Pro	Leu	His	Ala	Met	Pro	Ala	Thr	Asp	
				690					695					700		
ctt	tca	gcc	att	atg	ccc	agc	cag	ttg	agg	ccc	gtt	aca	tat	caa	gac	2342
Leu	Ser	Ala	Ile	Met	Pro	Ser	Gln	Leu	Arg	Pro	Val	Thr	Tyr	Gln	Asp	
			705					710					715			
ttt	gaa	aat	gct	ttc	tgc	aag	att	cag	cct	agc	ata	tct	caa	aag	gag	2390
Phe	Glu	Asn	Ala	Phe	Cys	Lys	Ile	Gln	Pro	Ser	Ile	Ser	Gln	Lys	Glu	
		720						725				730				
ctt	gat	atg	tat	gtt	gaa	tgg	aac	aaa	atg	ttt	ggg	tgc	agt	cag	tga	2438
Leu	Asp	Met	Tyr	Val	Glu	Trp	Asn	Lys	Met	Phe	Gly	Cys	Ser	Gln	*	
	735					740					745					
taacttcttt	ag															2450

<210> 243
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (168)..(437)

<400> 243	
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aagatgcctg taaatcaaatt ttcactataa ttgtaaagaa acctgaggca attagttaaa	120
aagttttaag tattcaggca attcatgata ccttggtgaa ataaagc atg cag act	176
	Met Gln Thr
	1
cat aaa aac ttg tat ata atc aaa ata aag ttc tac aaa tgg gaa aga	224
His Lys Asn Leu Tyr Ile Ile Lys Ile Lys Phe Tyr Lys Trp Glu Arg	
5 10 15	
gga tta tta tca ggg tat att aag gtg tta gac tta caa aag aag tgc	272
Gly Leu Leu Ser Gly Tyr Ile Lys Val Leu Asp Leu Gln Lys Lys Cys	
20 25 30 35	
ata att aat tac tca ttt aaa att aat tct ata ccc att agc ttg gca	320
Ile Ile Asn Tyr Ser Phe Lys Ile Asn Ser Ile Pro Ile Ser Leu Ala	
40 45 50	
aca gat aaa ata aaa gca tgc aac agt gct ttc tta gtc gac gcg gcc	368
Thr Asp Lys Ile Lys Ala Cys Asn Ser Ala Phe Leu Val Asp Ala Ala	
55 60 65	
gcg aat tcg gat cct cga gag atc tct ttt ttt ggg ttt ggt ggg gta	416
Ala Asn Ser Asp Pro Arg Glu Ile Ser Phe Phe Gly Phe Gly Gly Val	
70 75 80	

tct tca tca tcg aat aga tag ttatatacat catgctcttc aattaaaa	465
Ser Ser Ser Ser Asn Arg *	
85 90	

<210> 244
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (83)..(829)

<400> 244	
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gcgggccggc ctcggggcag cc atg gac tcg cag gaa ttg aag act ttg att	112
Met Asp Ser Gln Glu Leu Lys Thr Leu Ile	
1 5 10	
aat tac tat tgt caa gag aga tat ttc cat cat gta tta ctg gtt gcc	160
Asn Tyr Tyr Cys Gln Glu Arg Tyr Phe His His Val Leu Leu Val Ala	
15 20 25	
agt gaa gga att aag agg tat gga agt gat cca gtc ttc agg ttt tat	208
Ser Glu Gly Ile Lys Arg Tyr Gly Ser Asp Pro Val Phe Arg Phe Tyr	
30 35 40	
cat gcc tat ggc aca tta atg gaa ggt aaa act caa gaa gct ctt cga	256
His Ala Tyr Gly Thr Leu Met Glu Gly Lys Thr Gln Glu Ala Leu Arg	
45 50 55	
gaa ttt gag gct att aaa aat aaa caa gat gta tca ctt tgt tct cta	304
Glu Phe Glu Ala Ile Lys Asn Lys Gln Asp Val Ser Leu Cys Ser Leu	
60 65 70	
ctt gca ctg ata tat gcc cat aaa atg agt cct aat cca gat aga gaa	352
Leu Ala Leu Ile Tyr Ala His Lys Met Ser Pro Asn Pro Asp Arg Glu	
75 80 85 90	
gct att ctg gaa tca gat gcc aga gtg aag gaa caa cgt aaa gga gct	400
Ala Ile Leu Glu Ser Asp Ala Arg Val Lys Glu Gln Arg Lys Gly Ala	
95 100 105	
gga gag aaa gcc tta tac cat gca ggc tta ttt tta tgg cac att ggt	448
Gly Glu Lys Ala Leu Tyr His Ala Gly Leu Phe Leu Trp His Ile Gly	
110 115 120	
cgc cat gat aaa gca agg gaa tat att gac aga atg atc aaa ata tca	496
Arg His Asp Lys Ala Arg Glu Tyr Ile Asp Arg Met Ile Lys Ile Ser	
125 130 135	

gat ggt agt aaa cag gga cac gtt ttg aaa gca tgg ctt gat att aca	544
Asp Gly Ser Lys Gln Gly His Val Leu Lys Ala Trp Leu Asp Ile Thr	
140 145 150	
aga gga aaa gag cct tac act aaa aaa gca ctg aag tat ttt gaa gag	592
Arg Gly Lys Glu Pro Tyr Thr Lys Lys Ala Leu Lys Tyr Phe Glu Glu	
155 160 165 170	
gga ctc caa gat ggg aat gat act ttt gct ctg ctg ggt aag gca caa	640
Gly Leu Gln Asp Gly Asn Asp Thr Phe Ala Leu Leu Gly Lys Ala Gln	
175 180 185	
tgc ctt gag atg cgc cag aat tat tca ggt gcc ctg gag act gtg aac	688
Cys Leu Glu Met Arg Gln Asn Tyr Ser Gly Ala Leu Glu Thr Val Asn	
190 195 200	
cag ata atc gtg aat ttt ccg agc ttc ctt cct gct ttt gtt aag aaa	736
Gln Ile Ile Val Asn Phe Pro Ser Phe Leu Pro Ala Phe Val Lys Lys	
205 210 215	
atg aaa tta caa cta gcc ttg cag gat tgg gac cag aca gtt gag aca	784
Met Lys Leu Gln Leu Ala Leu Gln Asp Trp Asp Gln Thr Val Glu Thr	
220 225 230	
gca aaa ggt tgc tgc tcc aag ata gcc aaa atg tgg aag cac tga gaa	832
Ala Lys Gly Cys Cys Ser Lys Ile Ala Lys Met Trp Lys His *	
235 240 245	
tgcaggcact ctactatgtg tgtagagagg gggatataga gaaggcttcc accaagctgg	892
aaaacttggg aaatgcattg gatgccatgg aaccacagaa tgctcaactt ttctataaca	952
ttacactcgc cttcagcaga acttgtggac gtagtcaact tattcttcaa aaaattcaaa	1012
cgttacttga gagagctttt agtttaaccc tcagcaatca gaatttgcta cagacttgga	1072
taccaatt	1080

<210> 245
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)..(286)

<400> 245	
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ttcaatattg tagttaattt tttggctttc aacagcagcc ctagta atg gtg gag	115
	Met Val Glu
	1

ttg tta att aat gtg tat att gta ctg aat ttc tgt cag tta agg ggt	163
Leu Leu Ile Asn Val Tyr Ile Val Leu Asn Phe Cys Gln Leu Arg Gly	
5 10 15	
tca ctg ctt tgg tgg aaa ttg gtg gaa att gct agc agg ttc cac gat	211
Ser Leu Leu Trp Trp Lys Leu Val Glu Ile Ala Ser Arg Phe His Asp	
20 25 30 35	
gtt tat ttt ttt ctc cat gtt gta tat cat tac cat ttc aca tac gcg	259
Val Tyr Phe Phe Leu His Val Val Tyr His Tyr His Phe Thr Tyr Ala	
40 45 50	
ttt cta ttt ttc ttc ctc tcc tcc tga tctcc ttaaaaatga atctagagtt	311
Phe Leu Phe Phe Phe Leu Ser Ser *	
55 60	
gggtggctttt tccccctcct ctttggccag ttccacagtt cagttcttcc tgaaaacagg	371
gatgatgaac ttgtaggac aggacaaatg tgtgtttttc aaaaacttaa ggctgggtgt	431
gaaacacctt ctgtggacaa ggatttgtaa acttctctcc tccctccagc tgcggcccca	491
gcctaactga tagttacttg attcagtgtg ctagacactt aaatagcatc tatgtctctt	551
tcaaggggaat ttgtcaaata atgctgttta gctaattggt gcaagcaatt gcatattaac	611
agctgtgatt ttgttggaca gcaagtatta tggccaaagc cagtttcttg gcatttcaaa	671
aataatgcaa taaaaactag ttgaggttag ctgaggctgg aaatgccttt ttcattgtaa	731
atgattcact tctatatattt tctttctttt tctttttttt tcttttggtt tcatcctgga	791
ttcatccctt gatcttaaat caaaacgtca gatcaatgaa ctatgaacta aagtattttt	851
cttaagccta ttgagtgatt aattttttta aaaatgttta aatgcatatg cttttctttc	911
agcacaacaa acagcaaaaa cttttgtaat aactaactta cctttgcatg tatgaagaac	971
tgagtcattt atttccttaa cttactctc tttcaagtaa caggtggcag atcataaaat	1031
gaattcttta ttgtatctac aactccaca ttctttactg tgtcctacta ctgtatcttg	1091
gctccctgct gtattaaaca ccatcttaag cacttggtcc tgcaggactc cttcttgaca	1151
ttttgtctcc ccttcaaag tcaactcaaag agtgggactt catcaaaaaga aatgaattag	1211
tctctatcac accgaatact aagatttatt tcctctgatg gtacatagat ttctctctcc	1271
actaagaggg tcaactctcat agaggaaatgt cttgtcagtt ttatacttgc tgaggctaga	1331
ctgacaataa aaatgagctg ggcagttaaa ttagcatttg ttactatatt ggcctataaa	1391
ggatcagggt gatgataata cctctaaaaa tatgcaataa taaaacaata gttatgaaag	1451
aaacttgaaa ggtttgcaag gtttctccta tccctgttaa aattatcatt tattatctct	1511
ttgtcagtg tagtaaggta acccatgaca gaataatttg agtgatagtt catcatgcag	1571

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aggatatgat caagatatta cctaattggtt ttatcctgaa aaaggtgtat acttttaggg 1631
cactgttaac aatgcgagtg aaaccaagat ggtgcaagtt ccctttgcag atggcgtggg 1691
cacacttgat ttttattatg agtgaatgta atctttctgt attttaccag agttacagca 1751
attacctgaa aagtttccta acattttaat aatggttaggg atttcgtttt ggttttagtt 1811
gtcctcaaga gacaacaggt tcacagtaat ttccatgatg ttgggtgtgg ctaagctggg 1871
gattggttct gttccccctg ctcccgtgta gagaaaagct atatttatac tgcattcttt 1931
ctcaactttc aggtaaaaca aactatgatt taaaaaaga aaaaagaaaa gacaggtact 1991
tttacttcaa agagtgcctt gctacatttt tatttaaacc aaaaatcaaa taaaataagg 2051
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attccaaaaa aaaaaaa 2128

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<210> 246
<211> 3373
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (146) .. (2254)

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<400> 246
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tttccccaca gggtgactta aatgtcccag gctggaaggt ggagcgagaa gtggatgccc 120
ccagggctct gggtcacact ccagg atg act tct cgg aac cag ctg gtg cag 172
                               Met Thr Ser Arg Asn Gln Leu Val Gln
                               1 5
aag gtg ctg cag gag ctg cag gaa gca gtg gag tgc gaa ggc ctg gag 220
Lys Val Leu Gln Glu Leu Gln Glu Ala Val Glu Cys Glu Gly Leu Glu
10 15 20 25
ggg ctc ata ggt gct tcc ttg gag gcc aag cag gtc ctg tct tcc ttc 268
Gly Leu Ile Gly Ala Ser Leu Glu Ala Lys Gln Val Leu Ser Ser Phe
30 35 40
act ctc ccc acc tgc cgg gag gga ggc cct ggc ctc cag gtg ctg gaa 316
Thr Leu Pro Thr Cys Arg Glu Gly Gly Pro Gly Leu Gln Val Leu Glu
45 50 55
gtg gac tcg gtg gcc ctg agc ctg tat cca gaa gat gct cca cgg aac 364
Val Asp Ser Val Ala Leu Ser Leu Tyr Pro Glu Asp Ala Pro Arg Asn
60 65 70

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cgc tgg cgg cgg cag tcc cag gag cac cgg cag aag gtt gct gcc cgc Arg Trp Arg Arg Gln Ser Gln Glu His Arg Gln Lys Val Ala Ala Arg 300 305 310	1084
ttc tcc gcc aag cac ttc ctg cag gac agc ttc cac cgg ggg ggc gtc Phe Ser Ala Lys His Phe Leu Gln Asp Ser Phe His Arg Gly Gly Val 315 320 325	1132
gtg cca ctt cag cag ttc ctc cag cgg ttc ccg gag atc tcc cgc tca Val Pro Leu Gln Gln Phe Leu Gln Arg Phe Pro Glu Ile Ser Arg Ser 330 335 340 345	1180
acc tac tat gtc tgg aag cat gag ctg ctg ggc tct ggc acc tgc ccg Thr Tyr Tyr Val Trp Lys His Glu Leu Leu Gly Ser Gly Thr Cys Pro 350 355 360	1228
gcc ttg ccc ccc agg gag gtg ctg ggc atg gag gag cta gag aag ctg Ala Leu Pro Pro Arg Glu Val Leu Gly Met Glu Glu Leu Glu Lys Leu 365 370 375	1276
ccg gag gag cag gtg gct gag gag gag ctg gag tgc tcc gca ctg gcg Pro Glu Glu Gln Val Ala Glu Glu Glu Leu Glu Cys Ser Ala Leu Ala 380 385 390	1324
gtg tca agc cct gga atg gtc tta atg cag cgg gcc aag ttg tac ctg Val Ser Ser Pro Gly Met Val Leu Met Gln Arg Ala Lys Leu Tyr Leu 395 400 405	1372
gag cat tgc atc tcc ctg aac aca ctg gta ccc tat cgc tgc ttc aaa Glu His Cys Ile Ser Leu Asn Thr Leu Val Pro Tyr Arg Cys Phe Lys 410 415 420 425	1420
cgc agg ttc cct ggc atc tca cgg tcc act tat tat aat tgg cgg cga Arg Arg Phe Pro Gly Ile Ser Arg Ser Thr Tyr Tyr Asn Trp Arg Arg 430 435 440	1468
aag gcc ctc cgg agg aac ccc agc ttc aag ccg gca cca gcc ctc tct Lys Ala Leu Arg Arg Asn Pro Ser Phe Lys Pro Ala Pro Ala Leu Ser 445 450 455	1516
gct gct ggg act ccc cag cta gca tct gtt ggg gaa ggg gct gta att Ala Ala Gly Thr Pro Gln Leu Ala Ser Val Gly Glu Gly Ala Val Ile 460 465 470	1564
cct tgg aag agt gag gcg gaa gag ggg gca ggg aat gcc aca ggt gag Pro Trp Lys Ser Glu Ala Glu Glu Gly Ala Gly Asn Ala Thr Gly Glu 475 480 485	1612
gac cct ccc gcc ccc ggg gag ctc ctg cca cta agg atg ccc ctg tcc Asp Pro Pro Ala Pro Gly Glu Leu Leu Pro Leu Arg Met Pro Leu Ser 490 495 500 505	1660
cgt tgg cag agg cgt ctg cgc agg gct gcc cgc agg cag gtg ctg agt Arg Trp Gln Arg Arg Leu Arg Arg Ala Arg Arg Gln Val Leu Ser 510 515 520	1708
ggg cat ctc cct ttc tgc cgc ttc cgc ctc cgc tac ccc agc ctg tca	1756


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ttagaggggg gttggttagc tagagctgct ttcagctttt cctggagaca aaaggagtgt 2650
tatagcatga tcatcgggtcc cactgggcag aacgttatct tcagtttctt ttgggggttg 2710
gcatcctctt tactcagttg tttcccaaag gaacattagg ctggaatatg ggggccaggt 2770
gtggtggctt atgcctgtaa tcctagcgct ttgggaggcc aaggcaggag gatcacttga 2830
ggctaggagt tagagaccac cctgggcaat gtagtgagac ctcatctctt agaaaaaaaa 2890
aaagaaagaa aatcaaatgt agagctgac agcagcttgt gcctggcatc cccaaggag 2950
aaggtgccag gtcagcagga gcagcagcag ggatgtatag aaagaaccac agctggcctc 3010
taaaggatgg cactgaggca cggagatct tgaggcactg gagatcactg aggggctggc 3070
ctgtccctg caaggagtgt gggaccaggt ggggcaaggc tgggagatgc aggctctgtt 3130
tgcagattat ggcccagagt ctctgcttgt gggtgcttga tccacctgct gggacctgct 3190
agtctcggc cagcctggct gtcagttggg gattccacct ttctgctgag cgtcttctcg 3250
gagctggagg cccatcttca gtgagagatc acaaagcggc caggcagggtg ggagactgaa 3310
tttgcttgt tcgagagtaa cgtttgaaaa ccaaagaaat aaagtgatgc agtgcccaca 3370
aaa 3373

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<210> 247
<211> 817
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (90)..(662)

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<400> 247
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cagcctggcg gacgagcccc gcggcggag atg ggg gcg acg ggg gcg gcg gag 113
Met Gly Ala Thr Gly Ala Ala Glu
1 5
ccg ctg caa tcc gtg ctg tgg gtg aag cag cag cgc tgc gcc gtg agc 161
Pro Leu Gln Ser Val Leu Trp Val Lys Gln Gln Arg Cys Ala Val Ser
10 15 20
ctg gag ccc gcg cgg gct ctg ctg cgc tgg tgg cgg agc ccg ggg ccc 209
Leu Glu Pro Ala Arg Ala Leu Leu Arg Trp Trp Arg Ser Pro Gly Pro
25 30 35 40
gga gcc ggc gcc ccc ggc gcg gat gcc tgc tct gtg cct gta tct gag 257
Gly Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser Glu

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45	50	55	
atc atc gcc gtt gag gaa aca gac gtt cac ggg aaa cat caa ggc agt			305
Ile Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly Ser			
60	65	70	
gga aaa tgg cag aaa atg gaa aag cct tac gct ttt aca gtt cac tgt			353
Gly Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys			
75	80	85	
gta aag aga gca cga cgg cac cgc tgg aag tgg gcg cag gtg act ttc			401
Val Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe			
90	95	100	
tgg tgt cca gag gag cag ctg tgt cac ttg tgg ctg cag acc ctg cgg			449
Trp Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg			
105	110	115	120
gag atg ctg gag aag ctg acg tcc aga cca aag cat tta ctg gta ttt			497
Glu Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe			
125	130	135	
atc aac ccg ttt gga gga aaa gga caa ggc aag cgg ata tat gaa aga			545
Ile Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg			
140	145	150	
aaa gtg gca cca ctg ttc acc tta gcc tcc atc acc act gac atc atc			593
Lys Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile			
155	160	165	
gtt act gaa cat gct aat cag gcc aag gag act ctg tat gag att aac			641
Val Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn			
170	175	180	
ata gac aaa tac gac ggg tga gt aagccgtctt tcctcgccat caagtccatt			694
Ile Asp Lys Tyr Asp Gly *			
185	190		
gttaatgaaa aagttctacc cacctctcag ttttgagagc tccttttcct aaatccgccc			754
cccgctcca cccagacca attgtaaaag taaacatgct tcttacagga aggcaagaaa			814
gaa			817

<210> 248
 <211> 2416
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (526)..(1962)

 <400> 248

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actggtgggt tggaggctgt cgtgtggctg accagagatg gccagctgat gggtcacaca	180
gttggggatg gtgtcaggag gtcaacctga ccagcagaga cggctggcag gaaggtcacg	240
gaaggccagc caggcatggg gccactgggt gcaggcaggt ggcggatctg agtggcctga	300
cacattggat ggtcgcttat ttgggcagcg tgattgtcag aacagtgtgg caggggctgc	360
tgcagggagc catttgagaca tctgcagggc cccgccggag gcctcggatg gccacgtagg	420
gtctgcctat caagagaacc cccagatgat cacagtcccc cagagacagc cagacccccg	480
gggaccagc ctctcacagt cagtctccc acccgagtga ccccg	534
atg gcg gcc Met Ala Ala 1	
tcc cag ctg gcg gcg ctg gaa gga gtg gac tcc ggt ccc agg gtg ccc	582
Ser Gln Leu Ala Ala Leu Glu Gly Val Asp Ser Gly Pro Arg Val Pro	
5 10 15	
ggg gcc agc ccc ggc ttc cta tat tcc gag ggc cag cgg ctg gca ctg	630
Gly Ala Ser Pro Gly Phe Leu Tyr Ser Glu Gly Gln Arg Leu Ala Leu	
20 25 30 35	
gag gct ctg ttg agc aag ggc gcg gag gcg ttc cag acc tgc gtg cag	678
Glu Ala Leu Leu Ser Lys Gly Ala Glu Ala Phe Gln Thr Cys Val Gln	
40 45 50	
cgc gag gag ctg tgg ccc ttc ctc agt gcg gat gag gtt cag ggc ttg	726
Arg Glu Glu Leu Trp Pro Phe Leu Ser Ala Asp Glu Val Gln Gly Leu	
55 60 65	
gca gcg gca gct gaa gac tgg aca gtg gcc aag cag gag ccc agc ggg	774
Ala Ala Ala Ala Glu Asp Trp Thr Val Ala Lys Gln Glu Pro Ser Gly	
70 75 80	
atg gca gag gga gcc acc acc gcc gat gtg gac gcg ggc agc ctg agc	822
Met Ala Glu Gly Ala Thr Thr Ala Asp Val Asp Ala Gly Ser Leu Ser	
85 90 95	
tac tgg cct ggg cag tgc gag cag ccg gcg ccc gtc ctg cgg ctg ggc	870
Tyr Trp Pro Gly Gln Ser Glu Gln Pro Ala Pro Val Leu Arg Leu Gly	
100 105 110 115	
tgg cca gtg gac tct gcg tgg aaa ggc atc acc cgg gcg cag ctg tac	918
Trp Pro Val Asp Ser Ala Trp Lys Gly Ile Thr Arg Ala Gln Leu Tyr	
120 125 130	
acc cag cct cct gga gag ggt cag ccg ccc ctc aag gag ctg gtg cgg	966
Thr Gln Pro Pro Gly Glu Gly Gln Pro Pro Leu Lys Glu Leu Val Arg	
135 140 145	
ctg gag atc cag gct gcc cac aag ctg gtg gcc gtg gtc atg gac gtc	1014

Leu	Glu	Ile	Gln	Ala	Ala	His	Lys	Leu	Val	Ala	Val	Val	Met	Asp	Val	
		150					155					160				
ttc	act	gac	cca	gac	ctg	ctt	ttg	gac	ttg	gtg	gat	gct	gcc	acg	cgc	1062
Phe	Thr	Asp	Pro	Asp	Leu	Leu	Leu	Asp	Leu	Val	Asp	Ala	Ala	Thr	Arg	
	165					170					175					
cgc	tgg	gta	cct	gtc	tac	ctg	ctc	ctg	gac	cgc	cag	cag	ctg	cct	gcc	1110
Arg	Trp	Val	Pro	Val	Tyr	Leu	Leu	Leu	Asp	Arg	Gln	Gln	Leu	Pro	Ala	
180					185				190						195	
ttc	ctg	gaa	ctg	gcc	cag	cag	ctg	ggg	gtg	aac	ccc	tgg	aac	acg	gag	1158
Phe	Leu	Glu	Leu	Ala	Gln	Gln	Leu	Gly	Val	Asn	Pro	Trp	Asn	Thr	Glu	
				200					205					210		
aac	gtg	gat	gtc	cgt	gtc	gtg	cgg	ggc	tgc	agc	ttc	cag	agc	cgc	tgg	1206
Asn	Val	Asp	Val	Arg	Val	Val	Arg	Gly	Cys	Ser	Phe	Gln	Ser	Arg	Trp	
			215					220					225			
cga	cgg	cag	gtg	agc	ggc	acc	gtg	cgg	gag	aag	ttt	gtg	ctg	ctg	gac	1254
Arg	Arg	Gln	Val	Ser	Gly	Thr	Val	Arg	Glu	Lys	Phe	Val	Leu	Leu	Asp	
		230					235					240				
ggc	gag	agg	gtc	atc	tca	gga	tcc	tac	agc	ttc	acg	tgg	agt	gac	gca	1302
Gly	Glu	Arg	Val	Ile	Ser	Gly	Ser	Tyr	Ser	Phe	Thr	Trp	Ser	Asp	Ala	
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Pro	Pro	Ala	Pro	Pro	Gln	Lys	Pro	Ser	Val	Ile	Gly	Gly	Leu	Gln	Arg	
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atg gcc cct cgg ccc	
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Arg Ala Arg Pro Gly Val Ala Val Ala Cys Cys Trp Leu Leu Thr Val	
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Val Leu Arg Cys Cys Val Ser Phe Asn Val Asp Val Lys Asn Ser Met	
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Thr Phe Ser Gly Pro Val Glu Asp Met Phe Gly Tyr Thr Val Gln Gln	
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Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile Gly Ser Pro Leu Val	
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Gly Gln Pro Lys Asn Arg Thr Gly Asp Val Tyr Lys Cys Pro Val Gly	
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Arg Gly Glu Ser Leu Pro Cys Val Lys Leu Asp Leu Pro Val Asn Thr	
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Thr Glu Glu Val Leu Val Ala Ala Lys Lys Ile Val Gln Arg Gly Gly	
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Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val Lys Lys Val Met Val	
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Ile Lys Ser Tyr Phe Ser Ser Leu Asn Leu Thr Ile Arg Gly Glu Leu	
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Pro Trp Leu Leu Ser Trp Val Ser Ala Thr Ala Trp Arg Ala Ala Arg
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tggggccatg atggtagctg attgctaaat ttacataact cagttcatcg tcacaggagc			120
cctaagaggt tgatacgacc atgagtccat tttcactgag gaaaaccgaa gaaaagaaat			180
tgtaaattggc cagagatgta tggctggtga	atg gcc ctg tgt gga ggc agg		231
	Met Ala Leu Cys Gly Gly Arg		
	1 5		
gcc aag gtg aat gct cct gct atg cag atg atg cag ccc aga gag ccg			279
Ala Lys Val Asn Ala Pro Ala Met Gln Met Met Gln Pro Arg Glu Pro			
10 15 20			

cag cca cct ctg cga gtc cca cag ctg gaa gga gca ccc agt cct ccc 327
 Gln Pro Pro Leu Arg Val Pro Gln Leu Glu Gly Ala Pro Ser Pro Pro
 25 30 35

aca cta gcc gga cag gcc cgc agc ctg cac tac tga gctg tcacggagga 377
 Thr Leu Ala Gly Gln Ala Arg Ser Leu His Tyr *
 40 45 50

ctctaccaag cccagtgcg gagccacaag tggaggacat cctg 421

<210> 254
 <211> 636
 <212> DNA
 <213> Homo sapiens

<220>
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ggaggcctgg tgcactacac agctcctttg tgctccagg ccacctgccc aagctggtgt 180

gcctcccttc taaggctctg tcccactggg cacaggaggc agatccagca gcgtggaatc 240

ccagataac atg tcc cac aga ctc tgg caa cgt cac aga tca cat gga 288
 Met Ser His Arg Leu Trp Gln Arg His Arg Ser His Gly
 1 5 10

gag gca agt gca ggc caa cga cat ccg cat ccg ggt cct aca gga gga 336
 Glu Ala Ser Ala Gly Gln Arg His Pro His Pro Gly Pro Thr Gly Gly
 15 20 25

gaa cgg gcg gct cca atc aat gct gtc caa aat ccg gga agt ggc cca 384
 Glu Arg Ala Ala Pro Ile Asn Ala Val Gln Asn Pro Gly Ser Gly Pro
 30 35 40 45

gca ggg tgg cct caa ggt ggg cct gag agg gcg ggc cct tgg gga cca 432
 Ala Gly Trp Pro Gln Gly Gly Pro Glu Arg Ala Gly Pro Trp Gly Pro
 50 55 60

gga gga agc ccc tat cca gca gca ggt ctt cag act ctg ccc cgg gaa 480
 Gly Gly Ser Pro Tyr Pro Ala Ala Gly Leu Gln Thr Leu Pro Arg Glu
 65 70 75

ctt gtg gag agc cca cct cat cac atg agg cct tag gctg tgcttttggtg 530
 Leu Val Glu Ser Pro Pro His His Met Arg Pro *
 80 85

aaacattttt cacatttcca gaaggcgtga ggatgttatg gattcgatgc cttccagttc 590

cataagccct ttgtagctgt cattccttta agtgcagcaa caagcc

636

<210> 255
<211> 718
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (414) .. (695)

<400> 255

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caccccccaag cctggactgg aagtgtgttg agcccctggg tcaggctggc gagccagctc	120
ggccctgccc acccaggggt ttccgagatc acccctgggt aggcggcgtg ccagtccctt	180
gctttcttac ttgttctgca gagcggggag ctgaggctgc atgaggaag actcccgtac	240
cccagcacgg tggaggggtg gatgggggtca cgcctgtgcg acccaggagg tggccagcag	300
aaggaaacag tagtgtccac catggtctgc gtctccccac cacggattgt cttgggtccg	360
gatttgagac atggcagggc cagatgagga caacttgatg acagtttaca gag atg	416
	Met
	1
gag gca ggg tgc cag gaa gcc acg ggg gag ccc cca ggg cac tca gca	464
Glu Ala Gly Cys Gln Glu Ala Thr Gly Glu Pro Pro Gly His Ser Ala	
5 10 15	
gtc cag gca ggg ctg ggc gtc ctg gca agg agc agg gac ctt ctg ccc	512
Val Gln Ala Gly Leu Gly Val Leu Ala Arg Ser Arg Asp Leu Leu Pro	
20 25 30	
agg ggt gtg gcc agc ctg tgg gtg ctg tgt gca gga ccc cag gaa cca	560
Arg Gly Val Ala Ser Leu Trp Val Leu Cys Ala Gly Pro Gln Glu Pro	
35 40 45	
agg ccg cag tct ctt ccc tcg ctc cag cat cct ccc aag gcc acc ctt	608
Arg Pro Gln Ser Leu Pro Ser Leu Gln His Pro Pro Lys Ala Thr Leu	
50 55 60 65	
ggc tgc act cag cca gag agc tgg ggc aca ggg acc cca cag gtt tcc	656
Gly Cys Thr Gln Pro Glu Ser Trp Gly Thr Gly Thr Pro Gln Val Ser	
70 75 80	
ctg gag gct gtc agg ggc tcc ggt ggg ggc ggg ggg tga gcccgctggg	705
Leu Glu Ala Val Arg Gly Ser Gly Gly Gly Gly *	
85 90	
ttcactgcac ctc	718

<210> 256
 <211> 1767
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (251)..(1609)

<400> 256

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cagtttccac atctgcacaa tgggggtgac catccctgcc ctgctggctg ccaggagcgg      180
ctgtgagtct tcaggcgtgg atgcagcctg ggggaagcca tagggcgctt tcacaggcct      240
ggccttcacc  atg gcg gga ggg aga ccg cat ctg aag agg agt ttc tcc      289
              Met Ala Gly Gly Arg Pro His Leu Lys Arg Ser Phe Ser
                1             5             10

atc atc ccc tgc ttt gtc ttc gtg gag tgc gtg ctg ctg ggc att gtg      337
Ile Ile Pro Cys Phe Val Phe Val Glu Ser Val Leu Leu Gly Ile Val
   15             20             25

atc ctg ctt gct tac cgc ctg gag ttc acg gac acc ttc cct gtg cac      385
Ile Leu Leu Ala Tyr Arg Leu Glu Phe Thr Asp Thr Phe Pro Val His
   30             35             40             45

acc cag gga ttc ttc tgc tat gac agt acc tac gcc aag ccc tac cca      433
Thr Gln Gly Phe Phe Cys Tyr Asp Ser Thr Tyr Ala Lys Pro Tyr Pro
              50             55             60

ggg cct gag gct gcc agc cga gtg cct cct gct ctt gtc tac gca ctg      481
Gly Pro Glu Ala Ala Ser Arg Val Pro Pro Ala Leu Val Tyr Ala Leu
              65             70             75

gtc act gcc ggg ccc acc ctc acg atc ctg ctg gga gag ctg gcg cgt      529
Val Thr Ala Gly Pro Thr Leu Thr Ile Leu Leu Gly Glu Leu Ala Arg
   80             85             90

gcc ttt ttc cct gca cca cct tca gcc gtc cca gtc atc ggg gag agc      577
Ala Phe Phe Pro Ala Pro Pro Ser Ala Val Pro Val Ile Gly Glu Ser
   95             100            105

acc atc gtg tct ggg gcc tgc tgc cgc ttc agc ccc cca gtg cgg agg      625
Thr Ile Val Ser Gly Ala Cys Cys Arg Phe Ser Pro Pro Val Arg Arg
  110             115             120             125

ctg gtc cgc ttc ctg ggg gtc tac tcc ttc ggc ctc ttc acc acg acc      673
Leu Val Arg Phe Leu Gly Val Tyr Ser Phe Gly Leu Phe Thr Thr Thr
              130             135             140

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atc ttc gcc aac gcg ggg cag gtg gtg acc ggc aat ccc acg cca cac Ile Phe Ala Asn Ala Gly Gln Val Val Thr Gly Asn Pro Thr Pro His 145 150 155	721
ttc ctg tcc gtg tgc cgc ccc aac tac acg gcc ctg ggc tgc ctg cca Phe Leu Ser Val Cys Arg Pro Asn Tyr Thr Ala Leu Gly Cys Leu Pro 160 165 170	769
cct tct ccg gat cgg cca ggt ccc gac cgc ttt gtc act gac cag ggt Pro Ser Pro Asp Arg Pro Gly Pro Asp Arg Phe Val Thr Asp Gln Gly 175 180 185	817
gcc tgc gct ggc agt ccc agc ctc gtg gcc gcc gcg cgc cgc gcc ttc Ala Cys Ala Gly Ser Pro Ser Leu Val Ala Ala Ala Arg Arg Ala Phe 190 195 200 205	865
ccc tgc aag gat gcg gcc ctc tgc gcc tac gcg gtc acc tac aca gcg Pro Cys Lys Asp Ala Ala Leu Cys Ala Tyr Ala Val Thr Tyr Thr Ala 210 215 220	913
atg tac gtg act ctc gtg ttc cgc gtg aag ggc tcc cgc ctg gtc aaa Met Tyr Val Thr Leu Val Phe Arg Val Lys Gly Ser Arg Leu Val Lys 225 230 235	961
ccc tcg ctc tgc ctg gcc ttg ctg tgc ccg gcc ttc ctg gtg ggc gtg Pro Ser Leu Cys Leu Ala Leu Leu Cys Pro Ala Phe Leu Val Gly Val 240 245 250	1009
gtc cgc gtg gcc gag tac cga aac cac tgg tcg gac gtg ctg gct ggc Val Arg Val Ala Glu Tyr Arg Asn His Trp Ser Asp Val Leu Ala Gly 255 260 265	1057
ttc ctg aca ggg gcg gcc atc gcc acc ttt ttg gtc acc tgc gtt gtg Phe Leu Thr Gly Ala Ala Ile Ala Thr Phe Leu Val Thr Cys Val Val 270 275 280 285	1105
cat aac ttt cag agc cgg cca ccc tct ggc cga agg ctc tct ccc tgg His Asn Phe Gln Ser Arg Pro Pro Ser Gly Arg Arg Leu Ser Pro Trp 290 295 300	1153
gag gac ctg ggc caa gcc ccc acc atg gat agc ccc ctc gaa aag tta Glu Asp Leu Gly Gln Ala Pro Thr Met Asp Ser Pro Leu Glu Lys Leu 305 310 315	1201
agt gtg gcg cag gaa ccc gag gtc tgc agg ccg cat tcg aca ccg gca Ser Val Ala Gln Glu Pro Glu Val Cys Arg Pro His Ser Thr Pro Ala 320 325 330	1249
cgg ctc acc cca tcc aag tcg cag aac tgc gcc cgc cgt ggc cac ctg Arg Leu Thr Pro Ser Lys Ser Gln Asn Cys Ala Arg Arg Gly His Leu 335 340 345	1297
atc ccc agc tgt gtc tcc tcc agg gcc cca gcc atg tgt tcg tcg ccc Ile Pro Ser Cys Val Ser Ser Arg Ala Pro Ala Met Cys Ser Ser Pro 350 355 360 365	1345
cgt gtg ccc cgt cct cga ttg agg tct gag ccg acg ccc ttg ccc ctg	1393

Arg Val Pro Arg Pro Arg Leu Arg Ser Glu Pro Thr Pro Leu Pro Leu	
370 375 380	
ccc cta ccc ctg cca gcg ccc acc ccc agc cag ggc ccc tcg cct tcc	1441
Pro Leu Pro Leu Pro Ala Pro Thr Pro Ser Gln Gly Pro Ser Pro Ser	
385 390 395	
tcc cct gga cct ggg ggg cca ggc ggg ggt ggt gga cgt ggc cgg aag	1489
Ser Pro Gly Pro Gly Gly Pro Gly Gly Gly Gly Gly Arg Gly Arg Lys	
400 405 410	
ctg ctg ctg ccc acg ccc ctg ctg cgg gac ctg tac acc ctg agt gga	1537
Leu Leu Leu Pro Thr Pro Leu Leu Arg Asp Leu Tyr Thr Leu Ser Gly	
415 420 425	
ctc tat ccc tcc ccc ttc cac cgg gac aac ttc agc cct tac ctg ttt	1585
Leu Tyr Pro Ser Pro Phe His Arg Asp Asn Phe Ser Pro Tyr Leu Phe	
430 435 440 445	
gcc agc cgt gac cac ctg ctg tga ggcccgacca cccaccaga atctgcccag	1639
Ala Ser Arg Asp His Leu Leu *	
450	
tccccacttc ttccctgcc a cgcgtgtgtg tgcgtgtgcc acgtgagtgc caaagtcccc	1699
agcaccceaa gccagccaga cccagattgt attgcggccg ctgagaggat caaactacgt	1759
cgcggccca	1767

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 <212> DNA
 <213> Homo sapiens

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 <222> (379) .. (1332)

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caggaaaggg cccgaggggt aggttgact gcgggccagg acctaacgcg ggggtcgggc	120
cgctcaggt gcttgggagt cggggactcg aaggacgcaa gtgttgagct cgcgcccttc	180
tcgaagccgt ttgggcggac gctgggggtcc ttggggctcc gcccagggg gtggggctat	240
atgttcggac aatgaccggc cgtccttgcg gtcccgcccc ctccccgccc ccggaagccg	300
cggcctcgct gagtggccag ccgcccggcg cccaggcctg gggcaccgcg agtgccgaac	360
cttcggctgg acaccaag atg cct ggc gaa cag cag gca gag gaa gag gag	411
Met Pro Gly Glu Gln Gln Ala Glu Glu Glu Glu	
1 5 10	

gag gaa gag atg cag gag gag atg gtg ctg ctg gtg aag ggt gag gag	459
Glu Glu Glu Met Gln Glu Glu Met Val Leu Leu Val Lys Gly Glu Glu	
15 20 25	
gat gag ggt gag gag aag tat gag gtg gtg aaa ctc aag atc ccc atg	507
Asp Glu Gly Glu Glu Lys Tyr Glu Val Val Lys Leu Lys Ile Pro Met	
30 35 40	
gac aac aag gag gtc ccg ggc gag gcg ccc gcg ccg tcc gcc gac ccg	555
Asp Asn Lys Glu Val Pro Gly Glu Ala Pro Ala Pro Ser Ala Asp Pro	
45 50 55	
gcg cgt ccc cac gcg tgc ccc gac tgc ggc cgc gcc ttc gcg cgc cgc	603
Ala Arg Pro His Ala Cys Pro Asp Cys Gly Arg Ala Phe Ala Arg Arg	
60 65 70 75	
tcc acg ctg gcg aag cac gcg cgc acg cac acg ggc gaa cgg ccc ttc	651
Ser Thr Leu Ala Lys His Ala Arg Thr His Thr Gly Glu Arg Pro Phe	
80 85 90	
ggg tgc acc gag tgc ggg cgg cgc ttc tca cag aag tcg gcg ctg acc	699
Gly Cys Thr Glu Cys Gly Arg Arg Phe Ser Gln Lys Ser Ala Leu Thr	
95 100 105	
aaa cac ggc cgc acg cac acg ggc gag cgg ccc tac gag tgc ccc gag	747
Lys His Gly Arg Thr His Thr Gly Glu Arg Pro Tyr Glu Cys Pro Glu	
110 115 120	
tgc gac aaa cgc ttc tcg gcc gcc tcg aac ctg cgg cag cac cgg cgg	795
Cys Asp Lys Arg Phe Ser Ala Ala Ser Asn Leu Arg Gln His Arg Arg	
125 130 135	
cgg cac acg ggc gag aag ccg tac gca tgc gcg cac tgc ggc cgc cgc	843
Arg His Thr Gly Glu Lys Pro Tyr Ala Cys Ala His Cys Gly Arg Arg	
140 145 150 155	
ttc gcg cag agc tcc aac tac gca cag cac ctg cgc gtg cac acg ggc	891
Phe Ala Gln Ser Ser Asn Tyr Ala Gln His Leu Arg Val His Thr Gly	
160 165 170	
gag aag ccg tac gcg tgc ccg gac tgc gga cgc gcc ttt ggc ggc agc	939
Glu Lys Pro Tyr Ala Cys Pro Asp Cys Gly Arg Ala Phe Gly Gly Ser	
175 180 185	
tcg tgc ctg gcg cgc cac cga cgc acg cac acg ggc gag cgg ccc tac	987
Ser Cys Leu Ala Arg His Arg Arg Thr His Thr Gly Glu Arg Pro Tyr	
190 195 200	
gct tgc gcc gac tgc ggc acg cgc ttc gct cag agc tcg gcg ctg gcc	1035
Ala Cys Ala Asp Cys Gly Thr Arg Phe Ala Gln Ser Ser Ala Leu Ala	
205 210 215	
aag cac cgg cgc gtg cac acg ggc gag aag ccg cac cgc tgc gct gtg	1083
Lys His Arg Arg Val His Thr Gly Glu Lys Pro His Arg Cys Ala Val	
220 225 230 235	

tgt ggc cgt cgc ttc ggc cac cgc tcc aac ctg gcg gag cac gcg cgc Cys Gly Arg Arg Phe Gly His Arg Ser Asn Leu Ala Glu His Ala Arg 240 245 250	1131
acg cac aca ggc gag cgg ccc tac ccc tgc gcc gag tgc ggc cgc cgc Thr His Thr Gly Glu Arg Pro Tyr Pro Cys Ala Glu Cys Gly Arg Arg 255 260 265	1179
ttc cgc cta agc tcg cac ttc att cgc cac cga cgc gcg cac atg cgg Phe Arg Leu Ser Ser His Phe Ile Arg His Arg Arg Ala His Met Arg 270 275 280	1227
cgc cgc ctg tat att tgc gcc ggc tgc ggc agg gac ttc aag ctg ccc Arg Arg Leu Tyr Ile Cys Ala Gly Cys Gly Arg Asp Phe Lys Leu Pro 285 290 295	1275
cct ggc gcc acg gcc gcc act gcc acc gag cgt tgc ccg gag tgt gag Pro Gly Ala Thr Ala Ala Thr Ala Thr Glu Arg Cys Pro Glu Cys Glu 300 305 310 315	1323
ggc agc tga gtcccg agggctgcgg aggggcgcgc tggggcttcg acctggctgc Gly Ser *	1379
actaaccag gctcctctc gccccggcct ccgggtctgg gaaattgagg ggacggcagg	1439
cccggtgcc ctggaactgg gagacagga gaatcccctg ccgggggtccc tggaaacagt	1499
gcccaccca catcactaca ttccctcggc ccgtgttagt gaataaagta ttatatcctc	1559
acccacccg tgctgtgag tgaggtgggt gggagaggaa gaaagtggg gttctccagg	1619
ctcaggtgcc aagtgagttg tcaaggaacc aaatggggat gtaaacctaa aaggggttcc	1679
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aaaactgtaa taactactag ttaaagggtt taactgctt gttatgtaag cttaccacgc	1919
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cacttgaggt taggagttcg ataccagcct ggccaacatg gtgaaaccg gtctctacta	2039
aaaatacaaa aattaactgg gtgtggtggc gggcgctgt aatcccagct actgaggggg	2099
ctgaggcatg agaatcactt gaacctggga gacagaggtt gcaatgaacc gagatagtgc	2159
cattgcactc cggcctgggc aacagaggaa gactgcctca aacaacaaa aaacaacaaa	2219
ccaaacaaa ccaaaaaaat ctcaaagcga ttggacctag cagctcatgc ctgtaatctc	2279
cagcactttg ggagggcgag gcaggaggat ctcttgaagt caagagtttg agatcagcct	2339
ggagaacaaa gtgagacccc catctatt	2367

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 <211> 581
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (97)..(525)

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<400> 258
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tgagacaggt gttttaatca tcgtttttgc acccag  atg aac aag gag agg gca      114
                                     Met Asn Lys Glu Arg Ala
                                     1           5

ttc agg cat ggc gac ccg cct gag cca cct cca ggg gca aga gat gag      162
Phe Arg His Gly Asp Pro Pro Glu Pro Pro Pro Gly Ala Arg Asp Glu
                10                15                20

cag att tac ttt aga aag gac aac agc atc agc cac tgc cac agc ccc      210
Gln Ile Tyr Phe Arg Lys Asp Asn Ser Ile Ser His Cys His Ser Pro
                25                30                35

ccc cag atc atc tgt act ggc tgt cag aac agt cct gct gaa acg cca      258
Pro Gln Ile Ile Cys Thr Gly Cys Gln Asn Ser Pro Ala Glu Thr Pro
                40                45                50

atc aca cct gtc att cac tgc tct gcc cag gac tct tca gtg ggc tcc      306
Ile Thr Pro Val Ile His Cys Ser Ala Gln Asp Ser Ser Val Gly Ser
                55                60                65                70

cca gcg cta agc att tgg cct gac act cca ggc gcc atg tgc cct ggt      354
Pro Ala Leu Ser Ile Trp Pro Asp Thr Pro Gly Ala Met Cys Pro Gly
                75                80                85

ccc cac cta cct ctc cac tgc aaa ttc tgg cca tac acc cct gca ccc      402
Pro His Leu Pro Leu His Cys Lys Phe Trp Pro Tyr Thr Pro Ala Pro
                90                95                100

cca aac agt gca ctc cca tct cag tcc aca ttc tcc cct tac aac atg      450
Pro Asn Ser Ala Leu Pro Ser Gln Ser Thr Phe Ser Pro Tyr Asn Met
                105                110                115

att cat cca aga cca tgg att cgt ggc ctt aag ttt act tct ggt ctg      498
Ile His Pro Arg Pro Trp Ile Arg Gly Leu Lys Phe Thr Ser Gly Leu
                120                125                130

gac ttc tgt gtc agc tcc aga gta tag ttgtc tcaactgaccc cttcacttgg      550
Asp Phe Cys Val Ser Ser Arg Val  *
135                140

gtgccagaga aactggata ttccagaccc c      581

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<210> 259
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (39)..(317)

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 Met Gly Leu Gly Pro
 1 5

cct acc gac ggc cca gga ccc atc gac cca cga gtc ggt ccg gcc gcc 101
 Pro Thr Asp Gly Pro Gly Pro Ile Asp Pro Arg Val Gly Pro Ala Ala
 10 15 20

ggg tgc aca atg ggt ggc tcc tcc agc gtc gcc gct atg aag aaa gtg 149
 Gly Cys Thr Met Gly Gly Ser Ser Ser Val Ala Ala Met Lys Lys Val
 25 30 35

gtt caa cag ctg cgg ctg gag gcc gga ctc aac cgc gta aaa gtt tcc 197
 Val Gln Gln Leu Arg Leu Glu Ala Gly Leu Asn Arg Val Lys Val Ser
 40 45 50

cag gca gct gca gac ttg aaa cag ttc tgt ctg cag aat gct caa cat 245
 Gln Ala Ala Ala Asp Leu Lys Gln Phe Cys Leu Gln Asn Ala Gln His
 55 60 65

gac cct ctg ctg act gga gta tct tca agt aca aat ccc ttc aga ccc 293
 Asp Pro Leu Leu Thr Gly Val Ser Ser Ser Thr Asn Pro Phe Arg Pro
 70 75 80 85

cag aaa gtc tgt tcc ttt ttg tag 317
 Gln Lys Val Cys Ser Phe Leu *
 90

<210> 260
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 <212> DNA
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<220>
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 <222> (239)..(961)

<220>
 <221> misc_feature

<222> (1)...(1480)

<223> n = a,t,c or g

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acgccgcctt	tcgctacgcg	gaatttgcag	atcttccct	ggacctcagg	cctctccggc	180
tgtagtaggg	tggacgcttc	acataagctt	ctctgggtcga	acttacccga	atctccag	238
atg gcc gcg ctg cgt cga atg ctc cac ttg ccg agc ctg atg atg ggg	286					
Met Ala Ala Leu Arg Arg Met Leu His Leu Pro Ser Leu Met Met Gly						
1	5	10	15			
acg tgc cgc ccc ttt gcg ggc tca ctg gct gat agt tgc ctg gcg gac	334					
Thr Cys Arg Pro Phe Ala Gly Ser Leu Ala Asp Ser Cys Leu Ala Asp						
20	25	30				
cgc tgt ctc tgg gat cgg ctg cat gcc cag cct cgt ttg ggc act gtc	382					
Arg Cys Leu Trp Asp Arg Leu His Ala Gln Pro Arg Leu Gly Thr Val						
35	40	45				
ccc acc ttc gac tgg ttc ttt gga tac gac gaa gtc cag ggg ctc cta	430					
Pro Thr Phe Asp Trp Phe Phe Gly Tyr Asp Glu Val Gln Gly Leu Leu						
50	55	60				
ctg cca ttg ctg cag gag gca cag gct gcc agt cct ctg cga gtg ctg	478					
Leu Pro Leu Leu Gln Glu Ala Gln Ala Ala Ser Pro Leu Arg Val Leu						
65	70	75	80			
gat gtg ggc tgt ggg act tcc agc cta tgt aca ggc ctc tac acc aaa	526					
Asp Val Gly Cys Gly Thr Ser Ser Leu Cys Thr Gly Leu Tyr Thr Lys						
85	90	95				
tct cca cac cca gtg gat gtg ctg ggg gtg gac ttt tct cct gtg gct	574					
Ser Pro His Pro Val Asp Val Leu Gly Val Asp Phe Ser Pro Val Ala						
100	105	110				
gtg gcc cac atg aat agc ctc ctg gag ggt ggc cca agc caa aca cct	622					
Val Ala His Met Asn Ser Leu Leu Glu Gly Gly Pro Ser Gln Thr Pro						
115	120	125				
cta tgc cct gga cac cct gcc tca agc ctc cac ttc atg cac gcc gat	670					
Leu Cys Pro Gly His Pro Ala Ser Ser Leu His Phe Met His Ala Asp						
130	135	140				
gct cag aac ctg ggg gct gtg gct tct tca ggc tct ttc caa cta ctg	718					
Ala Gln Asn Leu Gly Ala Val Ala Ser Ser Gly Ser Phe Gln Leu Leu						
145	150	155	160			
ctg gac aaa ggc aca tgg gat gct gtt gcc cgg gga ggt ctg cct agg	766					
Leu Asp Lys Gly Thr Trp Asp Ala Val Ala Arg Gly Gly Leu Pro Arg						
165	170	175				
gct tac cag ctt cta tca gaa tgc ttg agg gtt cta aac cct cag ggg	814					
Ala Tyr Gln Leu Leu Ser Glu Cys Leu Arg Val Leu Asn Pro Gln Gly						

180	185	190	
acc ctg att cag ttc tca gat gag gac cct gat gtg cga ctg ccc tgc			862
Thr Leu Ile Gln Phe Ser Asp Glu Asp Pro Asp Val Arg Leu Pro Cys			
195	200	205	
ctg gaa caa ggg tcc tat ggc tgg act gtg act gtg cag gag cta ggc			910
Leu Glu Gln Gly Ser Tyr Gly Trp Thr Val Thr Val Gln Glu Leu Gly			
210	215	220	
ccg ttc agg ggc atc acc tac ttt gct tac ttg att caa ggc tct cat			958
Pro Phe Arg Gly Ile Thr Tyr Phe Ala Tyr Leu Ile Gln Gly Ser His			
225	230	235	240
taa agac attttagtag tcctgaccct agtattttctg tgggcaagga gagggctgaa			1015
*			
gaactgtctt tgcaagctat ctggctgcaa agtgagaatt tgagtcctgg cttccacatt			1075
tactagctgg gtgccatatt gctgaatggt tctgttcccc agtttactca tctgcagagt			1135
gagaataact tggagttacg gagattacat acaatgatgt gcgcaatatt tagcacaaaa			1195
tgaatgctga aaagagaagg tacaattggg tcattcccca gtttcaacta actggagctc			1255
ctaaaagcag cagacaggaa ctgaatcaaa acccctgcgc tgactgactt gtataatcta			1315
gtggcctaac ctgtaagcct cattnttgtc acctgtaaaa ggagattgta agaggatggg			1375
tataacgagc ttcataaacc tcgatgagat atttgagggg gagggaacaa tacttaccct			1435
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ttgaagatcg tgacgtcttg taactagcag tgtgtgcaca gaatcctact caaggaacgt			180
cttggcccag cgatgcaaag aactgaagtt tcaagctgga agagcctgta ttgtcctcac			240
aatagtatag aagaattcaa gagaggagag agagacagca ccgaatgaag actgtaaaag			300

aaaagaagga atgccagaga ttgagaaaat ctgccaagac taggagggtgta acccagagga 360

aaccgtcttc agggcctgtt tgctggct atg ctt cga gaa cct ggg gat ccc 412
Met Leu Arg Glu Pro Gly Asp Pro
1 5

gaa aaa tta ggg gaa ttt ctt cag aaa gac aat atc agc gtg cat tat 460
Glu Lys Leu Gly Glu Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr
10 15 20

ttc tgt ctt atc tta tct agt aag ctg cct cag agg ggc cag tcc aac 508
Phe Cys Leu Ile Leu Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn
25 30 35 40

aga ggt ttc cat gga ttt ctg cct gaa gac atc aaa aag gag gca gcc 556
Arg Gly Phe His Gly Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala
45 50 55

cgg gct tct agg aag atc tgc ttt gtg tgc aag aaa aag gga gct gct 604
Arg Ala Ser Arg Lys Ile Cys Phe Val Cys Lys Lys Lys Gly Ala Ala
60 65 70

atc aac tgc cag aag gat cag tgc ctc aga aac ttc cat ctg cct tgt 652
Ile Asn Cys Gln Lys Asp Gln Cys Leu Arg Asn Phe His Leu Pro Cys
75 80 85

ggc caa gaa agg ggt tgc ctt tca caa ttt ttt gga gag tac aaa tca 700
Gly Gln Glu Arg Gly Cys Leu Ser Gln Phe Phe Gly Glu Tyr Lys Ser
90 95 100

ttt tgt gac aaa cat cgc cca aca cag aac atc caa cat ggg cat gtg 748
Phe Cys Asp Lys His Arg Pro Thr Gln Asn Ile Gln His Gly His Val
105 110 115 120

ggg gag gaa agc tgc atc tta tgt tgt gaa gac tta tcc caa cag agt 796
Gly Glu Glu Ser Cys Ile Leu Cys Cys Glu Asp Leu Ser Gln Gln Ser
125 130 135

gtt gag aac atc cag agc ccg tgt tgt agt caa gcc atc tac cac cgc 844
Val Glu Asn Ile Gln Ser Pro Cys Cys Ser Gln Ala Ile Tyr His Arg
140 145 150

aag tgc ata cag aaa tat gcc cac aca tca gca aag cat ttc ttc aaa 892
Lys Cys Ile Gln Lys Tyr Ala His Thr Ser Ala Lys His Phe Phe Lys
155 160 165

tgt cca cag tgt aac aat cga aaa gag ttt cct caa gaa atg ctg aga 940
Cys Pro Gln Cys Asn Asn Arg Lys Glu Phe Pro Gln Glu Met Leu Arg
170 175 180

atg gga att cat att cca gac agg agg tgg tgc ctc att ctg tgt gct 988
Met Gly Ile His Ile Pro Asp Arg Arg Trp Cys Leu Ile Leu Cys Ala
185 190 195 200

act gcg gat ccc acg gaa ccc aca gga ctg ctc ctc tct tag atctaac 1037
Thr Ala Asp Pro Thr Glu Pro Thr Gly Leu Leu Leu Ser *
205 210

agtaagaaat gggagtgtga ggagtgttca cctgctgcag ccacagacta catacctgaa 1097
aactcagggg acatcccttg ctgcagcagc accttccacc ctgaggaaca tttctgcaga 1157
gacaacacct tggaagagaa tccgggcctt tcttggactg attggccaga accttcctta 1217
ttagaaaagc cagagtcctc tcgtggcagg aggagctact cctggagggtc caagggtgtc 1277
agaatcacta acagctgcaa aaaatccaag taacaccttc tgagtagctg ctgtcccaca 1337
caatagggta tgaagctgcg ctccctccatc gggtttgggg agggagcact ctgggactgt 1397
gagacaagga agcagggcca gcagtgcagc tatgagccaa gcaaagagaa gtctcagtgg 1457
agcatgagga gggagcagtc cagatgccaa caaggaaatg cgtttatggc tacaagagtg 1517
cctctgcttt ctctctctct cctcccacca aggattcttc caccttaatc ttgttttcat 1577
atgcctcttc ttacttcacc catgtttgtt gttatgcaaa taaagggttt ctctccaaaa 1637
aaaaaaaa 1645

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<211> 694
<212> DNA
<213> Homo sapiens

<220>
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gactgtgtcc aaaaagcaag taaaccact tcaagcacac aaatc atg gtg aag 174
Met Val Lys
1
acc aac atg tat cat aat gaa aag gtg aac ttt cat gtt gaa tgt aaa 222
Thr Asn Met Tyr His Asn Glu Lys Val Asn Phe His Val Glu Cys Lys
5 10 15
gac tat gta aaa aag gca aag gta aag atc aac cca gtg caa cag agc 270
Asp Tyr Val Lys Lys Ala Lys Val Lys Ile Asn Pro Val Gln Gln Ser
20 25 30 35
cgg ccc ttg ttg agc cag att cac aca gat gca gca aag gag aac acc 318
Arg Pro Leu Leu Ser Gln Ile His Thr Asp Ala Ala Lys Glu Asn Thr
40 45 50
tgc tac tgt ggt gca gtg gca aag aga caa gag aaa aaa ggg atg gag 366

Cys Tyr Cys Gly Ala Val Ala Lys Arg Gln Glu Lys Lys Gly Met Glu
55 60 65

cct ctt caa ggt cat gcc act ccc gct ttg cct ttt aaa gaa acc cag 414
Pro Leu Gln Gly His Ala Thr Pro Ala Leu Pro Phe Lys Glu Thr Gln
70 75 80

gaa cta tta cta agt ccc ctg ccc cag gaa ggt cct ggg tca ctt gca 462
Glu Leu Leu Leu Ser Pro Leu Pro Gln Glu Gly Pro Gly Ser Leu Ala
85 90 95

gca gga gag agc agc agt ctt tct gcc agt aca tca gtc tca gat tca 510
Ala Gly Glu Ser Ser Ser Leu Ser Ala Ser Thr Ser Val Ser Asp Ser
100 105 110 115

tcc cag aaa aaa gaa gag cac aat tat tct ctt ttt gtc tcc gac aac 558
Ser Gln Lys Lys Glu Glu His Asn Tyr Ser Leu Phe Val Ser Asp Asn
120 125 130

ttg ggt gaa cag cca act aaa tgc agt cct gaa gaa gat gag gag gac 606
Leu Gly Glu Gln Pro Thr Lys Cys Ser Pro Glu Glu Asp Glu Glu Asp
135 140 145

gag gag gat gtt gat gat gag gac cat gat gaa gga ttc ggc agt gag 654
Glu Glu Asp Val Asp Asp Glu Asp His Asp Glu Gly Phe Gly Ser Glu
150 155 160

cat tac atc att ata taa tgggtacttcc tcaagttgct gg 694
His Tyr Ile Ile Ile *

<210> 263
<211> 1540
<212> DNA
<213> Homo sapiens

<220>
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<222> (1033)..(1188)

<400> 263

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tccagatctc cactcttatg cgccagctgc agcagggttaa ggacagccag caggatgagc 120

tggatgacct cggtgagatg cgcagaaagg tcctggaatc cttgtctgac aagattcaga 180

agaagaagaa aaaaattctg agttctgtgg tggcggaaac ccagcgtccc tatgaagagg 240

ctctcctaca gaagatgtgg gaaagccagg acttcctgaa atgcatgcaa aggttcagag 300

aagtgcgtgg gcaaggaagg tgggtgtccc tgtagggaag cagtggatgg gcagtcccca 360

cggcctgtgg gaatgagtca ggcttctcct gatctggcgc tcaggaggte tctgattctg 420
 gtgttggcct ccttccttgc cggtgccatt actgtcactt gtctttcatc tgggaaggcg 480
 attggcactg acctaggcct tgcctcatta gccagcaatg ctggctaata acccatttac 540
 aaccatcacc aaacatcacc tattcagcca ttaaccaccg tgcattcttta ccccttgatt 600
 cttgttactg cccaccaccc attatcagtg ttaatgaact tcaccatcac tgccttcttg 660
 aattaatttt cattatcttg cctcttcact ggtttttaat gtgcatgccc ttcactatct 720
 ctgccagcct ccattcattc ccacgattga gcattccccg ccactttgta acctgtctcc 780
 attctccatg atccctcacc tgtttcagca ccactgaata ttgtcactaa cttggaagcc 840
 agccgcaccc tgcattggga agtccccctc ctggagtcca gcaagtccca gtgacagaac 900
 ccataccatt tccccagata gctttgctcc tcgttcattt tggcctttct ccttttggtt 960
 ggggggccatt tgcctctccc ttctcccctg ctgtgccttt cctctcagtt tattgaccag 1020
 tttgaggaga ac atg cct gta tta agg gcc gag gtg gaa gag ctc caa 1068
 Met Pro Val Leu Arg Ala Glu Val Glu Glu Leu Gln
 1 5 10
 gcc cag acc cgg gaa ccc cga gag gtc ata ttt gag gat gtt ctg ctt 1116
 Ala Gln Thr Arg Glu Pro Arg Glu Val Ile Phe Glu Asp Val Leu Leu
 15 20 25
 cgg aga ccc aag tgc acc cca gac atg gat gtc atc ctc aac att cct 1164
 Arg Arg Pro Lys Cys Thr Pro Asp Met Asp Val Ile Leu Asn Ile Pro
 30 35 40
 gtg gaa gag cca cta ccc ttc tag atggcagtgc catgggccgc cctccccctc 1218
 Val Glu Glu Pro Leu Pro Phe *
 45 50
 tgctctcttc ccagcacctg gagccttgga tcatttactt ccaggaccgg atctccattc 1278
 agaccctgat ctacagtctc cctgtccctt ctgcccttcc tccctctttc tttccctccc 1338
 tccctccctc ccttcttccc cccttccctt cctctctctt tcttctctcc tctccctccc 1398
 tccctccttt ctttcttctt gtgggtttttt cctctcttct tcccttcttt ctggttggtg 1458
 ctgctgggcc aggtgggaat ttctgattaa atctgtatt ccttttttac caataaagct 1518
 ggatttacat ttaaaaaaaaa aa 1540

<210> 264
 <211> 583
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (216)..(464)

<400> 264

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gtgctgagag gtgagtttagc tgcagaagaa atgctggaag ctggcaaaga tcagttcgtg      60
aggtttaaca agtcatttcc ataacataaa agtacaaagt gaagtagcaa ttgctgatgt      120
ggaatctgca gcaagcattt ccagaatatc tagataaatg gcagaggtag ctctactaga      180
gttttaacag agacaaaaca gccttacttc aggag   atg cca ttt agg act ttc      233
                                   Met Pro Phe Arg Thr Phe
                                   1               5

aca gct cta ggt aag cta ata tct gac ttc aaa gat tca aag gac ggg      281
Thr Ala Leu Gly Lys Leu Ile Ser Asp Phe Lys Asp Ser Lys Asp Gly
              10              15              20

ctg act ctt tac ttt gta gag aca gcg tca cgc tct gtt gtg ctg gct      329
Leu Thr Leu Tyr Phe Val Glu Thr Ala Ser Arg Ser Val Val Leu Ala
              25              30              35

ggt ctt gaa ctc ttg acc tca agt gat cct cca acc tca gcc tcc caa      377
Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Thr Ser Ala Ser Gln
              40              45              50

agc act gga att aca ggt gta agc cac ttt tcc cag cct ggg ctg gct      425
Ser Thr Gly Ile Thr Gly Val Ser His Phe Ser Gln Pro Gly Leu Ala
              55              60              65              70

ttc ttg tta gag gtc aat gca gtt ggt gac ttt aaa tga atgctaatat      474
Phe Leu Leu Glu Val Asn Ala Val Gly Asp Phe Lys  *
              75              80

tcaattacca ttccaaaaat ccaagagcca gttaagaatt atgctacatc ctcgtgccga      534

attcattgcc tcgagggcca aattccctat agtgatcgta ttaaattca      583

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<210> 265
 <211> 2077
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (154)..(834)

<400> 265

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cggcacgagg acagcataga ggaagtcaag gaagatagaa acaggcatcc tccagcaaac      60
ctgcccactc cagccagtac ccggattctt agaaaatatt ccaatattcg aggaaagctc      120

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agagcccagc aacgtttaat caagaatgag aaa atg gaa tgc cca gat gct ctg	174
Met Glu Cys Pro Asp Ala Leu	
1 5	
gct gtg gaa agt aag cca agt cgt aag agc gta tgc atc aac cct ctg	222
Ala Val Glu Ser Lys Pro Ser Arg Lys Ser Val Cys Ile Asn Pro Leu	
10 15 20	
atg tcc ccc aag ctt gcc ctg caa gtg gat gca gat ggg ttt cct gtt	270
Met Ser Pro Lys Leu Ala Leu Gln Val Asp Ala Asp Gly Phe Pro Val	
25 30 35	
aag ccc aag agt act gaa gga atg aag gga agg aag ggg aag cag gtg	318
Lys Pro Lys Ser Thr Glu Gly Met Lys Gly Arg Lys Gly Lys Gln Val	
40 45 50 55	
tct gaa atc ttg cct aaa gca gaa gtt cag agt aaa cgc aag aga aca	366
Ser Glu Ile Leu Pro Lys Ala Glu Val Gln Ser Lys Arg Lys Arg Thr	
60 65 70	
gaa ggc agc agc cct cca gat agt aag aac aag ggg cct acg gtg aaa	414
Glu Gly Ser Ser Pro Pro Asp Ser Lys Asn Lys Gly Pro Thr Val Lys	
75 80 85	
gcc agc aaa gaa aag cat gct gat gga gcc acc aaa acc cct gct gcc	462
Ala Ser Lys Glu Lys His Ala Asp Gly Ala Thr Lys Thr Pro Ala Ala	
90 95 100	
aag agg cca gct gca agg gac aga agc agc caa ccc ccc aaa aag acg	510
Lys Arg Pro Ala Ala Arg Asp Arg Ser Ser Gln Pro Pro Lys Lys Thr	
105 110 115	
tct ttg aaa gag aat aaa gtg aag atc cct aaa aag tcc gct ggg aag	558
Ser Leu Lys Glu Asn Lys Val Lys Ile Pro Lys Lys Ser Ala Gly Lys	
120 125 130 135	
agc tgc cct ccc tcc agg aaa gaa aaa gag aat aca aac aaa agg cct	606
Ser Cys Pro Pro Ser Arg Lys Glu Lys Glu Asn Thr Asn Lys Arg Pro	
140 145 150	
tcc cag tct att gcc tcg gaa aca ctg acg aaa cct gca aaa cag aag	654
Ser Gln Ser Ile Ala Ser Glu Thr Leu Thr Lys Pro Ala Lys Gln Lys	
155 160 165	
ggg gcc ggt gaa tcc tct tca agg cct cag aaa gcc acg aat agg aag	702
Gly Ala Gly Glu Ser Ser Ser Arg Pro Gln Lys Ala Thr Asn Arg Lys	
170 175 180	
cag agt agt gga aag act cgg gcc aga ccc tca acg aaa acc cca gag	750
Gln Ser Ser Gly Lys Thr Arg Ala Arg Pro Ser Thr Lys Thr Pro Glu	
185 190 195	
agc agt gca gct cag aga aag cga aag ctg aag gca aag ctg gac tgt	798
Ser Ser Ala Ala Gln Arg Lys Arg Lys Leu Lys Ala Lys Leu Asp Cys	
200 205 210 215	
tcg cac ggc aaa cgg agg cgg ctg gat gca aag tga ttgg aaagatggta	848

Ser His Gly Lys Arg Arg Arg Leu Asp Ala Lys *

220

225

gccaagagta aaactgttct atagaagtaa ccttttatct tgcattaact aaatctgctt 908
 ttataagctt atcaagcctt tcaaatttac agttaatgga gaacaccgta atttgagatg 968
 tcagaaaatg catctcagat ggagaaggga acttgcagag tccttctctg aggctaaggg 1028
 aagttatata ttatattctg gttgttcctt gggttttaaa cttggaacca agcagttttc 1088
 gtttttaaaa gtacagtgcc ttatttatcc tttttgtttt taaatttaca aaagctaaaa 1148
 agctgatcta tgtgattaaa ggcttgtatt ttatacttga tgcacaagca cttgtactgt 1208
 agccgagaag accaccatca tgcacataaa aggagctttt cagcagccac cctgcagcat 1268
 ctgcccacga acagatgccc ttctttgcaa accccagcag tgaacttccc tctctgtctt 1328
 gtttggttgt ttagatgatg tttgaaagct aaaccaaadc attttatggt atgcagagga 1388
 ttataatta taaaagatta ctatttctgt taccctctt taaaaaagat catgttcatt 1448
 gttggtcct cctctcacct ttgatgtttt gtcatttgag agcatgtatt ctaaattatg 1508
 tgcccatggg acaagagata tgcacaagt gttaattttt gtttacaac tctaaaaaat 1568
 catttgcac cccaaactgt attactaatt ctaccatct tcttcatttc tgggtcttgc 1628
 agcactcctg caaggcttcc atcctacttc gggaggaaaa agcctaggat ttttttttcc 1688
 catctttag ctgtaatttg atgattagga tgaaaatgac tcttattttc tttcttacc 1748
 agagtacttc catattcaaa gaaagccgaa ctattatttc cagtaataga aagggttaag 1808
 aatatgtatg tccatgtgtg tttgggtgca tttgcatgtg gttatcagcc acaaagtgtc 1868
 cccaatccca attttacagt aaaatttttt ccctatgcag tgtgcttggg tgtccctgag 1928
 ttgagtaatt agcaaaggac agatgggtta aaagtagccc agtgtctctg tgagcatccc 1988
 caataccact ttggtaccag actcagaaag atctaaaaca gcatggagtt atgtaaaggt 2048
 tagagcagcc ttgcagttgg aggaagcag 2077

<210> 266
 <211> 1175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(685)

<400> 266
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cgcaggcagg actctgggac agacgcaggc cagctgcccc gagcccagac caagc atg 118
Met
1
gac gcc gtg gat gcc acc atg gag aaa ctc cgg gca cag tgc ctg tcc 166
Asp Ala Val Asp Ala Thr Met Glu Lys Leu Arg Ala Gln Cys Leu Ser
5 10 15
cgc ggg gcc tcg ggc atc cag ggc ctg gcc agg ttt ttc cgc caa cta 214
Arg Gly Ala Ser Gly Ile Gln Gly Leu Ala Arg Phe Phe Arg Gln Leu
20 25 30
gac cgg gac ggg agc aga tcc ctg gac gct gat gag ttc cgg cag ggt 262
Asp Arg Asp Gly Ser Arg Ser Leu Asp Ala Asp Glu Phe Arg Gln Gly
35 40 45
ctg gcc aaa ctc ggg ctg gtg ctg gac cag gcg gag gca gag ggt gtg 310
Leu Ala Lys Leu Gly Leu Val Leu Asp Gln Ala Glu Ala Glu Gly Val
50 55 60 65
tgc agg aag tgg gac cgc aat ggc agc ggg acg ctg gat ctg gag gag 358
Cys Arg Lys Trp Asp Arg Asn Gly Ser Gly Thr Leu Asp Leu Glu Glu
70 75 80
ttc ctt cgg gcg ctg cgg ccc ccc atg tcc cag gcc cgg gag gct gtc 406
Phe Leu Arg Ala Leu Arg Pro Pro Met Ser Gln Ala Arg Glu Ala Val
85 90 95
atc gca gct gca ttt gcc aag ctg gac cgc agt ggg gac ggc gtc gtg 454
Ile Ala Ala Ala Phe Ala Lys Leu Asp Arg Ser Gly Asp Gly Val Val
100 105 110
acg gtg gac gac ctc cgc ggg gtg tac agt ggc cgt gcc cac ccc aag 502
Thr Val Asp Asp Leu Arg Gly Val Tyr Ser Gly Arg Ala His Pro Lys
115 120 125
gtg cgc agt ggg gag tgg acc gag gac gag gtg ctg cgc cgc ttc ctg 550
Val Arg Ser Gly Glu Trp Thr Glu Asp Glu Val Leu Arg Arg Phe Leu
130 135 140 145
gac aac ttc gac tcc tct gag aag gac ggg cag gtc aca ctg gcg gaa 598
Asp Asn Phe Asp Ser Ser Glu Lys Asp Gly Gln Val Thr Leu Ala Glu
150 155 160
ttc cag gac tac tac agc ggc gtg agt gcc tcc atg aac acg gat gag 646
Phe Gln Asp Tyr Tyr Ser Gly Val Ser Ala Ser Met Asn Thr Asp Glu
165 170 175
gag ttc gtg gcc atg atg acc agt gcc tgg cag ctg tga gcagctccgg 695
Glu Phe Val Ala Met Met Thr Ser Ala Trp Gln Leu *
180 185 190
ctcagccctg ctgccctggc ctgtcactcc ccaccctgc cggagacctc ccttccttg 755

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gcccttctc tcctgggcag ccacaccaca gagcggggag gggcaggtgg gggaatggag      815
gctgcaggac tggctagacc aggtccctgc cgggccacca ggcggaggtg ggacaaaggt      875
cctaacagga gtcactggct caggaccca gggagaaacg ctctcccccac ccacgccatg      935
ctgaccagag gtcttgacgc cctgtggat gccccgccg aggtcccccg atccccgcac      995
ccggactgct gtcctctgcc cctcccttgc gggccccca ggaagccagg tgaccccagg     1055
tgggaggctg tgtgtggagg ccatcctgga aggaagtta gacctgcca ggtgtggagc     1115
gaggggcaca ggggcacct aacctcagaa actgaaataa agcctttgaa aaaaaaaaaa     1175

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<210> 267
<211> 1094
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (116)..(604)

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<400> 267
cccacgcgtc cgtccactag caacagtctc ccagggcaca acacagctaa cacaaggccc      60
cgaggcagg actctgggac agacgcaggc cagctgcca gagcccagac caagc atg      118
                                     Met
                                     1
gac gcc gtg gat gcc acc atg gag aaa ctc cgg gca cag tgc ctg tcc      166
Asp Ala Val Asp Ala Thr Met Glu Lys Leu Arg Ala Gln Cys Leu Ser
                    5                      10                      15
cgc ggg gcc tcg ggc atc cag ggc ctg gcc agg ttt ttc cgc caa cta      214
Arg Gly Ala Ser Gly Ile Gln Gly Leu Ala Arg Phe Phe Arg Gln Leu
                    20                      25                      30
gac cgg gac ggg agc aga tcc ctg gac gct gat gag ttc cgg cag ggt      262
Asp Arg Asp Gly Ser Arg Ser Leu Asp Ala Asp Glu Phe Arg Gln Gly
                    35                      40                      45
ctg gcc aaa ctc ggg ctg gtg ctg gac cag gcg gag gca gag ggt gtg      310
Leu Ala Lys Leu Gly Leu Val Leu Asp Gln Ala Glu Ala Glu Gly Val
                    50                      55                      60                      65
tgc agg aag tgg gac cgc aat ggc agc ggg acg ctg gat ctg gag gag      358
Cys Arg Lys Trp Asp Arg Asn Gly Ser Gly Thr Leu Asp Leu Glu Glu
                    70                      75                      80
ttc ctt cgg gcg ctg cgg ccc ccc atg tcc cag gcc cgg gag gct gtc      406
Phe Leu Arg Ala Leu Arg Pro Pro Met Ser Gln Ala Arg Glu Ala Val
                    85                      90                      95

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atc gca gct gca ttt gcc aag ctg gac cgc agt ggg gac ggc gtc gtg      454
Ile Ala Ala Ala Phe Ala Lys Leu Asp Arg Ser Gly Asp Gly Val Val
      100                      105                      110

acg gtg gac gac ctc cgc ggg gtg tac agt ggc cgt gcc cac ccc aag      502
Thr Val Asp Asp Leu Arg Gly Val Tyr Ser Gly Arg Ala His Pro Lys
      115                      120                      125

gtc aca ctg gcg gaa ttc cag gac tac tac agc ggc gtg agt gcc tcc      550
Val Thr Leu Ala Glu Phe Gln Asp Tyr Tyr Ser Gly Val Ser Ala Ser
      130                      135                      140                      145

atg aac acg gat gag gag ttc gtg gcc atg atg acc agt gcc tgg cag      598
Met Asn Thr Asp Glu Glu Phe Val Ala Met Met Thr Ser Ala Trp Gln
      150                      155                      160

ctg tga gcagctccgg ctgagccctg ctgccctggc ctgtcactcc ccaccctgc      654
Leu *

cggagacctc ccttccttgg gccccttctc tcctgggcag ccacaccaca gagcggggag      714

gggcaggttg gggaatggag gctgcaggac tggctagacc aggtccctgc cggtcacca      774

ggcggaggtg ggacaaaggt cctaacagga gtcactggct caggacccca gggagaaacg      834

ctctccccac ccacgccatg ctgaccagag gtcttgagc ccctgtggat gccccgccg      894

aggtcccccg atccccgcac ccggactgct gtcctctgcc cctcccttgc gggccccca      954

ggaagccagg tgacccagg tgggaggctg tgtgtggagg ccattcctgga aggaagtta      1014

gacctgcca ggtgtggagc gaggggcaca ggggcatcct aacctcagaa actgaaataa      1074

agcctttgaa aaaaaaaaaa      1094

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<210> 268
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (169)..(387)

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ggatgtgttg tcctgggtgag cgattgtcct gtggcgctccg ggaccgagtt tgtggcccag      120

ggttatgtgt gcacttcaca cctctgactt ttttcagggt tcctattg atg gtt agg      177
                      Met Val Arg

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agc agg att tcg ggg atg aag gcg gca gca gca aga gga ggc tgc gac 225
 Ser Arg Ile Ser Gly Met Lys Ala Ala Ala Ala Arg Gly Gly Cys Asp
 5 10 15

tgc gga ccc cag att cgt ccc cct cca cca cac aca acg cca aga cgg 273
 Cys Gly Pro Gln Ile Arg Pro Pro Pro Pro His Thr Thr Pro Arg Arg
 20 25 30 35

gcc cca gga ggg cgt gaa gag aag act tcc ttt cct ctc ctc tcg cct 321
 Ala Pro Gly Gly Arg Glu Glu Lys Thr Ser Phe Pro Leu Leu Ser Pro
 40 45 50

cct ggc gct ggc cgt atg aag gtg tct ccc aga agc att agc aga gga 369
 Pro Gly Ala Gly Arg Met Lys Val Ser Pro Arg Ser Ile Ser Arg Gly
 55 60 65

gcc ctg tgg gag aaa tga ggagtg acccaaaaga aacttgctca aggacagcct 423
 Ala Leu Trp Glu Lys *
 70

ccttaaagca gacttccata taccccaacc tgcaaaagaa gactttacgt gaaatgttac 483

ag 485

<210> 269
 <211> 1170
 <212> DNA
 <213> Homo sapiens

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 <222> (168)..(611)

<220>
 <221> misc_feature
 <222> (1)...(1170)
 <223> n = a,t,c or g

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 tgagttctga cccctggagg agccactgtg gaagcagagc aatcgcc atg gag ttt 176
 Met Glu Phe
 1

gtg atg aag cag gct cta gga ggg gcc acc aag gac atg ggg aag atg 224
 Val Met Lys Gln Ala Leu Gly Gly Ala Thr Lys Asp Met Gly Lys Met
 5 10 15

ctg ggg ggt gac gag gag aag gac cca gac gcc gcc aag aag gag gag 272
 Leu Gly Gly Asp Glu Glu Lys Asp Pro Asp Ala Ala Lys Lys Glu Glu
 20 25 30 35

gag cgg cag gag gcg ctg cgc cag gcg gag gag gag cgc aag gcc aag Glu Arg Gln Glu Ala Leu Arg Gln Ala Glu Glu Glu Arg Lys Ala Lys 40 45 50	320
tac gcc aag atg gag gcg gag cgc gag gcc gtg cgc cag ggc atc cga Tyr Ala Lys Met Glu Ala Glu Arg Glu Ala Val Arg Gln Gly Ile Arg 55 60 65	368
gac aag tac ggc atc aag aag aag gag gag cgc gag gcc gag gcc cag Asp Lys Tyr Gly Ile Lys Lys Lys Glu Glu Arg Glu Ala Glu Ala Gln 70 75 80	416
gcc gcc atg gag gcc aac tcc gag ggg agc ttg acg cgg ccc aag aag Ala Ala Met Glu Ala Asn Ser Glu Gly Ser Leu Thr Arg Pro Lys Lys 85 90 95	464
gcc atc ccg ccg ggc tgc ggg gac gag gtg gag gag gag gac gag agc Ala Ile Pro Pro Gly Cys Gly Asp Glu Val Glu Glu Glu Asp Glu Ser 100 105 110 115	512
atc ctg gac acc gtc atc aag tac ctg ccc ggg ccg ctg cat gac atg Ile Leu Asp Thr Val Ile Lys Tyr Leu Pro Gly Pro Leu His Asp Met 120 125 130	560
ctc aag atg tat ccc cgc gcg gga cag ctg ccc cgc gga gcc ggc cat Leu Lys Met Tyr Pro Arg Ala Gly Gln Leu Pro Arg Gly Ala Gly His 135 140 145	608
tga acac tgcaccctcc acaggagccg cagaggccct gaggcaccgg actgcttgga *	665
gaccctgcgc ccctgcccag cacctcctcc gtgggcagct cctcggtgtg gggcctgcgg	725
ggttccctgc ggcgcagccg ggcgcgtgtg tggcctaatac cacctggttg ccctgcgggg	785
cggcatccga gcccctgttt ctctccatt catgtttatt ttgcatcaca atttgttgaa	845
tctcaggtag atgaggtctt tgcatttagt gagttttatc ttgacagggc gcgctcgccc	905
ccggtccctt tcgtccacat caaaaatgca tcacgtctcc acgtgtttcg ggccagggcg	965
gggcttgga ttgaccttca tgaccttaca tagctttaga gaagccataa cgcttgactg	1025
caatactaac gaccgacgcc cctccggaca gagaccacg cgcacctctg cgcacctcg	1085
acgctgtccg cggngacgtc gctgaccgcc ctgctcgccc tgagccctct cactgacttc	1145
tcccgggtcg tgtcttatta aaact	1170

<210> 270
<211> 1116
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (497) .. (766)

<400> 270

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actgtgtgca ttgcccgtct gtgaccgttt tcgactcaca gaaatggcag tctgaagtgg      120
ctcggcctct tgcttgagag acagattgga gcagagtctt tgtggatgca aagccacctg      180
ggccactgcc gtgtgtgcca ccctgaactt caagctgccc tgaaccgcgt gcgttttctca      240
gtgtcacgta cagctcggcc tgaccgtttg ctttttagtg ttctcttcct tctcgggtgc      300
ctctctctct tcctcactaa cattcatcca gagcctttca gtgcagaaat caggtagctg      360
ctgaactcgg cagctgcgtc ctttttccca tcatctcttc tgtcctttgc tagctgtcat      420
ttcttccttc ttggcttcaa ctgcacatcc ctgggtttgt cctaataagg aatttttccc      480
acttgagtag acaagc      atg aga ata tca tta ttt tta tat gtt ata tgt      529
                        Met Arg Ile Ser Leu Phe Leu Tyr Val Ile Cys
                        1           5           10

tat att ttt agc aga gaa aaa agt gga aaa tgt gtg caa act tgc aga      577
Tyr Ile Phe Ser Arg Glu Lys Ser Gly Lys Cys Val Gln Thr Cys Arg
                        15           20           25

agg ccc ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc      625
Arg Pro Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly
                        30           35           40

ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc ccc gga      673
Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly Pro Gly
                        45           50           55

gga ggg tcg tcc ctg tgc cca tgc ggt cag aaa ggc ccc gga gga ggg      721
Gly Gly Ser Ser Leu Cys Pro Cys Gly Gln Lys Gly Pro Gly Gly Gly
                        60           65           70           75

tca tct ctg tgc cca tgc ggt cag gtt ggg gct gag gca ctt tga tca      769
Ser Ser Leu Cys Pro Cys Gly Gln Val Gly Ala Glu Ala Leu *
                        80           85           90

ttgctcctcc tcagagtgtt cttttcctgc cctctcagat tataataacg aggtagttac      829
agagtgagct ccagcctaga tcgtctgggt ttgaatccag ctccatgact gtggccgtgt      889
tgcctaattct ctctgagtct cagcttcctt ttctgtaaag tgggtataat agtagagtct      949
acactgtggg gctgtgggtg gattcattgt gttcacacgt gtgcagggct gagaacaggg      1009
cccaaacag ggtaggcaca atgaagcatg agtcagaata ataatacaga tgacagtttc      1069
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tctatcacta atttgaacat tgcagacagt gcaaagaaga aaattag

1116

<210> 271
<211> 2569
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (15)..(596)

<400> 271

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	Met Asp Ala Val Val Pro Asp Arg Asn Ser Arg Val	
	1 5 10	
gac cca cgc gtc cgg ttt ccc agc gcg gtg ccc gcc cct cat cct cct	98	
Asp Pro Arg Val Arg Phe Pro Ser Ala Val Pro Ala Pro His Pro Pro		
	15 20 25	
cca gtc tcc ctc ccc tcg ccg act gcc gcc cca ggc tcc gcc atg ggg	146	
Pro Val Ser Leu Pro Ser Pro Thr Ala Ala Pro Gly Ser Ala Met Gly		
	30 35 40	
aat gtg cca tcc gcg gtg aag cac tgc ctc agc tac cag cag ctt ctc	194	
Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln Leu Leu		
	45 50 55 60	
cgg gag cat ctc tgg atc ggg gat tca gtg gca ggg gcg ctc gac ccc	242	
Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu Asp Pro		
	65 70 75	
gcg cag gaa aca tcc cag tta tct gga ctc cct gag ttt gtt aaa ata	290	
Ala Gln Glu Thr Ser Gln Leu Ser Gly Leu Pro Glu Phe Val Lys Ile		
	80 85 90	
gta gaa gtt ggg cct agg gat gga ttg cag aat gaa aag gtt ata gtt	338	
Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val Ile Val		
	95 100 105	
cct aca gat ata aaa att gaa ttt atc aat cga ctt tcc caa act ggc	386	
Pro Thr Asp Ile Lys Ile Glu Phe Ile Asn Arg Leu Ser Gln Thr Gly		
	110 115 120	
ttg tct gta ata gaa gtg act agc ttt gtg tct tcc aga tgg gta cca	434	
Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp Val Pro		
	125 130 135 140	
cag gtt gct gct gga gct act gag ata tca gtt ttt gga gct gca tct	482	
Gln Val Ala Ala Gly Ala Thr Glu Ile Ser Val Phe Gly Ala Ala Ser		
	145 150 155	
gaa tcc ttt agc aag aag aat att aac tgt tcc att gaa gaa agt atg	530	
Glu Ser Phe Ser Lys Lys Asn Ile Asn Cys Ser Ile Glu Glu Ser Met		

	160	165	170	
	gga aaa ttt gag gag gtt gtt aag tct gca aga cac atg aat att cca			578
	Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn Ile Pro			
	175	180	185	
	gca cga ggg tac tta tga aatccc acaaattctg ttttgtaa gtttattgtt			632
	Ala Arg Gly Tyr Leu *			
	190			
	aaagcttact caaaaattat ctagagattc ttatatcatt tataaaaata tacatagaat			692
	atcatatttc tattttgttt aatcagggta atcactatat agttacatct cattaacatc			752
	actgctgatt attagtgagt atctagcttg tggaatgtgt catgcaattg aaatcagagg			812
	tactagcatg caaatctggc attattaact attttattaa cactctagca cccaaatgca			872
	gccctcttat ctgagcctac atgtgctgat aagttgggtat aaactcacia cagcttttgg			932
	aaaagaatca cctaattgtg ttttcaaatt ttttttaaaa catgactttt tcttcaaaga			992
	gtattttatg tagaacttca atagaatata gcagatataa aattgagctg ctctgggaaa			1052
	tcattttatc cattctttct cccctcaat ggctgacttt tctacttcct ctgggtgatc			1112
	ccaaagcacc tccatagtat cttgcagaac actgtttaaa aatacttgat aaattgctta			1172
	tagaagataa atataaactt tcagttctct actattttct attatatgtg atttctataa			1232
	atntagagat atcagagata tcaatccctt tctcctcgcc ttgccttttt cttgtggaaa			1292
	cttatcagct gttcattcta agagatgttg attacaggac atggaaaata aaaactgacc			1352
	caagatccac aaacctaatt ttctctctca ggagtttaga aatgggtatac caaacatggg			1412
	tacttgtatt gaaagattat gtgattttgt cactgagttc actatttttg ggttcctagg			1472
	atggagccac atgcaaacca gtgacaggac agagtagtag aaagcagaaa tggaaaaagg			1532
	aggctcctag cggatgatgag aggtatgggg gagggaggag agggaaaaat ctgccttggg			1592
	gcttgtctgc ttccaggacc aatagttgcc tcaagtatta taaccaggcc tatgtgctgt			1652
	gaaacctata atgcattttt gtgtgtgttt gtttcttaag gaagaatttg tttctaagac			1712
	attagctact ttttctatta attttataaa tatggagata tgatgaacac acatcttaac			1772
	aagttaaagt gcatagcgat tggtaataga aggttgaaaag ctgggggatgg atttggtg			1832
	aggctgtact tcccttagtt gaggtgagca aagttcatgg tagcgggaaa gattcaacag			1892
	ttaatgagaa agataagtga gtcaattgtg actgaaaata ttagtgaaat gattggaatt			1952
	tcaatcaagg tgttttgggg gaacaattag agttagacta tacctagtaa aatattttgt			2012
	tagtttgttt tctatttata ttttctctgt cctccatagt aagtctacat gagtttctaa			2072

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aatttgaaat tacttttgta attaagatag atgcatatca tgtaaggact atatgagaaa 2132
aattttaaatt ccaaggcaat gtacttccaa agacataaaa taaaggatat ttattttttca 2192
ggcaaaaagtt acaaaaaccac aatcaaaaag gagagatata ctattgggttt ctcaattcga 2252
atataaataa gttgtctcaa ttttctttta aataaagaga aagatgaaga ccctatttcta 2312
cttcaatatg tgttttaaagt gtggagtata agcttttaaag taatttctcat tgggaagtta 2372
aaaagtatgt gactataaga agtaaatgct ttatgtagct tgctcttcaa ataggaaggg 2432
tttttttagt gttgaaagat ggatgcaaata ataagttgta ggaagtaacc ttttattatc 2492
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ctcttaaaaa aaaaaaa 2569

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<210> 272
<211> 1204
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (64) .. (630)

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<400> 272

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tttcgtaaatt agttgctccg tgggctttcc gcatttcacc ctgctccagg cagcgtggtc 60
tgt  atg gct ccg ccc tgg gca gga gga gaa aga aga ggg cca ggc acc 108
    Met Ala Pro Pro Trp Ala Gly Gly Glu Arg Arg Gly Pro Gly Thr
      1             5             10             15

acg tgc ctg cac tct ccc tgg atg ctg gag gct gct ccg ccg tgg gca 156
Thr Cys Leu His Ser Pro Trp Met Leu Glu Ala Ala Pro Pro Trp Ala
      20             25             30

gga gga gaa gga aga gaa ctg ggt gcc gcc tgc ctg cac tct ctc cgg 204
Gly Gly Glu Gly Arg Glu Leu Gly Ala Ala Cys Leu His Ser Leu Arg
      35             40             45

atg ctg gag gct gga ggc agt gag gca gca aca gcg cga ggg cga ggc 252
Met Leu Glu Ala Gly Gly Ser Glu Ala Ala Thr Ala Arg Gly Arg Gly
      50             55             60

gac ttt gga gct gcc tca tgc agc gac ctc gcc ttc cgc tgc gcc tcc 300
Asp Phe Gly Ala Ala Ser Cys Ser Asp Leu Ala Phe Arg Cys Ala Ser
      65             70             75

tcc cag aac cca aga agc ctg gaa cct gtg gcg tcc agc cct gaa agg 348
Ser Gln Asn Pro Arg Ser Leu Glu Pro Val Ala Ser Ser Pro Glu Arg
      80             85             90             95

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agg aga cgg caa ccc agc cgc gct ttt gcc tgc act ctc cct gga tgc      396
Arg Arg Arg Gln Pro Ser Arg Ala Phe Ala Cys Thr Leu Pro Gly Cys
      100                      105                      110

tgg agg ctg gag gca gtg acg cag caa cag cgc gag gcg act ttg gag      444
Trp Arg Leu Gln Ala Val Thr Gln Gln Gln Arg Glu Ala Thr Leu Glu
      115                      120                      125

cgg cct cat ata gcg acc tcg cct tcc gct gcg cgt cct ccc aga gcc      492
Arg Pro His Ile Ala Thr Ser Pro Ser Ala Ala Arg Pro Pro Arg Ala
      130                      135                      140

caa gaa gcc cgg aac ctg tgg cat cca tct ctg aaa gga gaa gac ggc      540
Gln Glu Ala Arg Asn Leu Trp His Pro Ser Leu Lys Gly Glu Asp Gly
      145                      150                      155

aac cca gcc gag gca cta ctg ggt tgg ggt ctc cac gac cga gct ggt      588
Asn Pro Ala Glu Ala Leu Leu Gly Trp Gly Leu His Asp Arg Ala Gly
      160                      165                      170                      175

ctc atc aag tgg cgt cca aca agg ggc tca aac ccg ggt tga ggggttg      637
Leu Ile Lys Trp Arg Pro Thr Arg Gly Ser Asn Pro Gly *
      180                      185

ctggagcgcac ggagaacgtg gaactacact ggaggacacc agagtactct taagcaatcc      697

cttgccaaaa accagcaact gatttggata ccatcaagac acctgaaatc ttgtcatgag      757

ccagatactg aggaagagat tttgggaaga acccaaggac cccccagttg cagccatgtc      817

aagactgaca ataaggaaga catcagtccc agcaagcaac attcatcggg cacagccacc      877

catgtggggc cagatcaaga agttgacaca gacggcggaa gaaaatctga agaaagcgga      937

tgaccagcta caatgagtaa tctaattgta gctatgatgg ctgtgctcac cattgccatg      997

agtattcccc cagcacctgc tgaaacaaaa aacattatac ttattgggca tatattcctt     1057

ttccaccagt ttcattggcca gtgacatggt tagaccccc agtggaggta tacactaatg     1117

atagcttttg gatacctggt tctacagatg atagaggccc atctcacccc caaaaggagg     1177

gaacattatg aatatttcgt tgggatt                                           1204

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<210> 273
 <211> 943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (356)..(610)

<220>
 <221> CDS
 <222> (27) .. (488)

<400> 274

aatttaggtg acactataga agagct atg acg tcg cat gca cgc gta cgt aag	53
Met Thr Ser His Ala Arg Val Arg Lys	
1 5	
ctt gga tcc tct aga gcg gcc gct gtc gtt gtt ctg agg aga aac ctt	101
Leu Gly Ser Ser Arg Ala Ala Ala Val Val Val Leu Arg Arg Asn Leu	
10 15 20 25	
aca agt gta ata aat gtg cga agg ttt tta atc aaa aag gaa tcc ttg	149
Thr Ser Val Ile Asn Val Arg Arg Phe Leu Ile Lys Lys Glu Ser Leu	
30 35 40	
cac aac atc aga gag ttc ata ctg gag aga aac ctt aca agt gta atg	197
His Asn Ile Arg Glu Phe Ile Leu Glu Arg Asn Leu Thr Ser Val Met	
45 50 55	
aat gtg gca agg ttt tta atc aaa aag caa gcc ttg caa aac atc aga	245
Asn Val Ala Arg Phe Leu Ile Lys Lys Gln Ala Leu Gln Asn Ile Arg	
60 65 70	
gag ttc ata ctg cag aga aac ctt aca agt gta atg agt gtg gca aag	293
Glu Phe Ile Leu Gln Arg Asn Leu Thr Ser Val Met Ser Val Ala Lys	
75 80 85	
cct tta ctg gac agt caa cac tta ttc acc atc aag caa tcc atg ggt	341
Pro Leu Leu Asp Ser Gln His Leu Phe Thr Ile Lys Gln Ser Met Gly	
90 95 100 105	
gta ggg aaa ctt tac aaa tgt aat gat tgt cac aaa gtc ttc agt aat	389
Val Gly Lys Leu Tyr Lys Cys Asn Asp Cys His Lys Val Phe Ser Asn	
110 115 120	
gct aca acc att gca aat cat tac aga atc cat att gaa gag aga tct	437
Ala Thr Thr Ile Ala Asn His Tyr Arg Ile His Ile Glu Glu Arg Ser	
125 130 135	
aca agt gta ata aat gtg gca aat ttt tca gac gtc att cat aac ttg	485
Thr Ser Val Ile Asn Val Ala Asn Phe Ser Asp Val Ile His Asn Leu	
140 145 150	
tag ttca tcagtgaact catactggag agaaacctta caaatatcat gactgtgaca	542
*	
aggtcttcag tcaagcttca tcctatgcaa aacatagaat tcatacagga gagaaacctc	602
acaagtgtga tgattgtggc aaagccttta cttcatgttc acacctcatt agacatcaga	662
gaattcatac tggacagatg ccttacaaat gtaagggtgg caaggtcttc actctgtggt	722
cattccatgc agaacatcag aaaattcatt tttagagataa ttgttccaaa taaaatgaat	782

ataaaaaaatc aaaaaaaaaa a

803

<210> 275
<211> 1078
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (357)..(713)

<220>
<221> misc_feature
<222> (1)...(1078)
<223> n = a,t,c or g

<400> 275

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gtgaatgaca tgggagacag acctgggggtc ttttagggac ggaaagcctc agccaagacc	120
cagactccca ggggtcatcaa cctcctcggg tctaataccc tccccagtgt ctgtctaccc	180
ctaagtccag agaacacgtc ctctctaggc tcgagccgga atcaatatag gctacaaggg	240
catcagttca ggctgcgcgg aggagagaag gaagtgctga tgtggagtcc tccctcccc	300
ttctccttca cccccaagtg tctcccacga ctgccctccc cgacctctag ctgacc	356
atg gca tca gag gca gaa aaa aca ttc cat cgg ttt gct gcg ttt gga	404
Met Ala Ser Glu Ala Glu Lys Thr Phe His Arg Phe Ala Ala Phe Gly	
1 5 10 15	
gaa tca tca agc agt ggc act gaa atg aac aac aag aac ttc tcc aag	452
Glu Ser Ser Ser Ser Gly Thr Glu Met Asn Asn Lys Asn Phe Ser Lys	
20 25 30	
ctg tgc aaa gac tgt ggc atc atg gat ggc aag aca gtc acc tcc acg	500
Leu Cys Lys Asp Cys Gly Ile Met Asp Gly Lys Thr Val Thr Ser Thr	
35 40 45	
gac gtg gac atc gtg ttc agc aaa gtc aag gcc aag aac gcc cga acc	548
Asp Val Asp Ile Val Phe Ser Lys Val Lys Ala Lys Asn Ala Arg Thr	
50 55 60	
atc acg ttt caa cag ttc aaa gag gca gtg aag gaa ctg ggc cag aag	596
Ile Thr Phe Gln Gln Phe Lys Glu Ala Val Lys Glu Leu Gly Gln Lys	
65 70 75 80	
cgc ttc aaa ggg aag agt cca gat gaa gtc ctg gag aac att tat gga	644
Arg Phe Lys Gly Lys Ser Pro Asp Glu Val Leu Glu Asn Ile Tyr Gly	
85 90 95	
ctc atg gag ggc aaa gac cca gcc acc act ggc gct act ttt ccc tgg	692
Leu Met Glu Gly Lys Asp Pro Ala Thr Thr Gly Ala Thr Phe Pro Trp	

100	105	110	
tta cct atg caa gaa acc tga aa gtgacccctag acccctccac ctccccaatc			745
Leu Pro Met Gln Glu Thr *			
115			
ccagctacgg ggaggcggtc ctgcatggtg gttaagatca aggcttttga gtgaaacaga			805
ccaggaattg aatcctgcct ctgcagctta caaactgcac accatctatc tgtttacgaa			865
accactgaaa gcttccttgt ttcattctgtt catgaggata gtatttttta ctcacggcag			925
tatgaggatc cattaagatg tatatcaaga gtttttagac cagtgcccg cacaatgtgga			985
tgctctcgtc tcgcctggac agcacacaca ctccaactcc agtaagactc aactcaaata			1045
tatctcttat acaacttcaa gaaaaaaaaaaa aaa			1078

<210> 276
 <211> 724
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (74)..(223)

<400> 276			
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cacctatgta aaa atg tca aaa ttg aaa atg cgg agg ggg cat ctg gaa			109
Met Ser Lys Leu Lys Met Arg Arg Gly His Leu Glu			
1 5 10			
tca aac tgg tgg cct ctc ggt ctg cag tct tat gct cta acc ctg agc			157
Ser Asn Trp Trp Pro Leu Gly Leu Gln Ser Tyr Ala Leu Thr Leu Ser			
15 20 25			
tat acc cct tcc tgc tgc tgt ggg ggt caa tta atg cct ttg act tgt			205
Tyr Thr Pro Ser Cys Cys Cys Gly Gly Gln Leu Met Pro Leu Thr Cys			
30 35 40			
gcg gtc aca ccc aga tga ccagtc acctgtgtgt tgccacttca caatggaagc			259
Ala Val Thr Pro Arg *			
45 50			
tcctaggagc tgccaggtct acctcagtga aaactcattg accttgtgca tagcaagagg			319
cagtccccgc tcctcagata acccccgtgc ctgtgtcttc cctgccttga gtccttagtt			379
atgggcagca ggctggaaaa gcactgccag cagccactag aatggccttg agagtcatcc			439
tccagtaact gtttatgggtg ggcacatata agagaaactt tgtgtgactg aggtgtctgt			499

tctaaaacac ttaatgacag agttgggcct ggctctcctg gtccagtgtt ccattcaggg 559
cagattcagc acaactgcag tctaggacaa aagatgattc tttcaacttt tacttcttca 619
gttaatacaa atgaagaatg ttagagaagg agcaactcca agaaatagtg agaagtgtgt 679
agctgagtag atttcccaaa agcattaata gggccagtgt tacca 724

<210> 277
<211> 1007
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119)..(682)

<400> 277
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cgcttgggct gccggacggt gggaacggaa gtcgctgtgg gacgctgagg aagccagg 118
atg gcg act ccg agc aag aag acg tca act cca agc ccc cag cct tcc 166
Met Ala Thr Pro Ser Lys Lys Thr Ser Thr Pro Ser Pro Gln Pro Ser
1 5 10 15
aag aga gct ctc ccg aga gac cct tcg tcg gag gtc ccg agc aag agg 214
Lys Arg Ala Leu Pro Arg Asp Pro Ser Ser Glu Val Pro Ser Lys Arg
20 25 30
aag aat tcg gcc ccg cag ctg ccg ctg ttg cag tcg tcc ggg cct ttc 262
Lys Asn Ser Ala Pro Gln Leu Pro Leu Leu Gln Ser Ser Gly Pro Phe
35 40 45
gtg gaa ggc tct atc gtc cgc atc tcg atg gag aac ttc cta aca tat 310
Val Glu Gly Ser Ile Val Arg Ile Ser Met Glu Asn Phe Leu Thr Tyr
50 55 60
gat att tgt gaa gta tct cct gga ccc cac ttg aat atg atc gtt gga 358
Asp Ile Cys Glu Val Ser Pro Gly Pro His Leu Asn Met Ile Val Gly
65 70 75 80
gcc aat gga aca ggg aag tcg agc att gtg tgt gcc att tgc ctt ggt 406
Ala Asn Gly Thr Gly Lys Ser Ser Ile Val Cys Ala Ile Cys Leu Gly
85 90 95
tta gct gga aaa cct gct ttc atg gga cga gca gat aag gtt ggg ttt 454
Leu Ala Gly Lys Pro Ala Phe Met Gly Arg Ala Asp Lys Val Gly Phe
100 105 110
ttt gtg aag aga gga tgt tct aga ggc atg gtt gaa att gaa ttg ttc 502
Phe Val Lys Arg Gly Cys Ser Arg Gly Met Val Glu Ile Glu Leu Phe
115 120 125
agg gct tct gga aat ctt gta atc acc cgt gag att gat gtg gca aaa 550

ttattgagat acgcgggggtt gcgacttggc ggcgggagcc aagcgcttga gctgtcactg 389
gagtgggttga gaggtggggg aaggacaggg tatggtggag tgggggtgggt 439

<210> 279
<211> 1771
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (24) .. (1049)

<400> 279
tttcgtcacg ggccttgttc acc atg tcg gtg ctg gat gcg ctt tgg gag 50
Met Ser Val Leu Asp Ala Leu Trp Glu
1 5

gat cgg gat gtc cgt ttc gac ctg tcc gcg cag caa atg aaa aca aga 98
Asp Arg Asp Val Arg Phe Asp Leu Ser Ala Gln Gln Met Lys Thr Arg
10 15 20 25

cct gga gaa gtc ctt att gat tgt tta gat tcc att gaa gac acc aaa 146
Pro Gly Glu Val Leu Ile Asp Cys Leu Asp Ser Ile Glu Asp Thr Lys
30 35 40

gga aat aat gga gat aga ggt aga ctc ttg gta aca aat tta aga att 194
Gly Asn Asn Gly Asp Arg Gly Arg Leu Leu Val Thr Asn Leu Arg Ile
45 50 55

ctc tgg cac tct ttg gca tta tca aga gtc aat gtt tct gtc ggt tac 242
Leu Trp His Ser Leu Ala Leu Ser Arg Val Asn Val Ser Val Gly Tyr
60 65 70

aat tgc ata ttg aat att aca aca agg act gct aac tct aaa tta cga 290
Asn Cys Ile Leu Asn Ile Thr Thr Arg Thr Ala Asn Ser Lys Leu Arg
75 80 85

ggc caa act gaa gct ctc tat ata cta aca aaa tgt aac agt act cgt 338
Gly Gln Thr Glu Ala Leu Tyr Ile Leu Thr Lys Cys Asn Ser Thr Arg
90 95 100 105

ttt gaa ttt ata ttt aca aat ttg gtt cct gga agc cct aga ctt ttt 386
Phe Glu Phe Ile Phe Thr Asn Leu Val Pro Gly Ser Pro Arg Leu Phe
110 115 120

act tct gtg atg gca gta cac aga gct tat gaa act tct aaa atg tat 434
Thr Ser Val Met Ala Val His Arg Ala Tyr Glu Thr Ser Lys Met Tyr
125 130 135

cgt gat ttt aaa tta aga agt gca cta att cag aac aag caa cta aga 482
Arg Asp Phe Lys Leu Arg Ser Ala Leu Ile Gln Asn Lys Gln Leu Arg
140 145 150

ctg ttg cca caa gaa cat gta tat gat aaa ata aat gga gtt tgg aat Leu Leu Pro Gln Glu His Val Tyr Asp Lys Ile Asn Gly Val Trp Asn 155 160 165	530
tta tcc agt gat cag ggc aat tta gga acc ttt ttt att acc aat gtg Leu Ser Ser Asp Gln Gly Asn Leu Gly Thr Phe Phe Ile Thr Asn Val 170 175 180 185	578
aga att gtg tgg cat gca aat atg aat gat agt ttt aat gtc agt ata Arg Ile Val Trp His Ala Asn Met Asn Asp Ser Phe Asn Val Ser Ile 190 195 200	626
cca tat ctg caa att cgt tca ata aag att aga gat tca aaa ttt ggt Pro Tyr Leu Gln Ile Arg Ser Ile Lys Ile Arg Asp Ser Lys Phe Gly 205 210 215	674
tta gct ctt gtc ata gaa agc tct cag cag agt ggt gga tat gtt ctt Leu Ala Leu Val Ile Glu Ser Ser Gln Gln Ser Gly Gly Tyr Val Leu 220 225 230	722
ggc ttt aaa ata gat cct gtg gaa aaa cta caa gaa tca gtt aag gaa Gly Phe Lys Ile Asp Pro Val Glu Lys Leu Gln Glu Ser Val Lys Glu 235 240 245	770
atc aat tca ctt cac aaa gtc tat tct gcc agt ccc ata ttt gga gtt Ile Asn Ser Leu His Lys Val Tyr Ser Ala Ser Pro Ile Phe Gly Val 250 255 260 265	818
gat tat gag atg gaa gaa aag ccc cag ccg ctc gaa gct ctg aca gtc Asp Tyr Glu Met Glu Glu Lys Pro Gln Pro Leu Glu Ala Leu Thr Val 270 275 280	866
gaa caa att caa gat gat gta gaa ata gac tct gat ggt cac acg gat Glu Gln Ile Gln Asp Asp Val Glu Ile Asp Ser Asp Gly His Thr Asp 285 290 295	914
gct ttt gtg gct tat ttt gct gat ggc aat aag caa caa gat cgt gaa Ala Phe Val Ala Tyr Phe Ala Asp Gly Asn Lys Gln Gln Asp Arg Glu 300 305 310	962
cct gta ttt tca gaa gaa ctg ggg ctt gca ata gag aaa ttg aag gat Pro Val Phe Ser Glu Glu Leu Gly Leu Ala Ile Glu Lys Leu Lys Asp 315 320 325	1010
gga ttc acc cta cag gga ctt tgg gaa gta atg agt tga ttgacctga Gly Phe Thr Leu Gln Gly Leu Trp Glu Val Met Ser *	1059
330 335 340	
gttgagatgg atttctatta aagatatctc tagtttaaag atactagtca cctgccataa	1119
gtcatggaat agtttttata ttacagctt ttatatattaa aacttgtaag agttttttta	1179
atgattgagg aaaaagtcatt tagaaaaact tcagtttttcg gccagcgcgt cgagggaggg	1239
gccagcgaca catggcctag taaccgtccg gccgcggcgc tggcttaagc catggctgag	1299

ggtagccgga ttcctcaggc cggggcgctc ctacagcagt gcctgcacgc ccggctgcaa 1359
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 atctacgtgt gctttttcaa gggagctgat aaagaacttc ttcccaaaat ggatctacga 1479
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 gactcttggt gaacagctcc tgtctttggt gaacagctcc ccagggcctc ctacccgcaa 1599
 actgcttgct aagaatctag ccatacttta tagtattgga gacacattct ccgttcatga 1659
 agcaatcgat aaatgtaatg atcttattcg tagcaaagat gattctccaa gttatcttcc 1719
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<210> 280
 <211> 1109
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (162)..(1064)

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 cggttcgacg atttcgttgc gcgttcgga actggtttcc cggaaggatt atgtctgcgc 120
 cctcgatccg accggaagtt gcacgtgag ccgcggacac c atg cag tgc gat 173
 Met Gln Ser Asp
 1
 gat gtt atc tgg gat aca cta gga aac aag caa ttt tgt tcc ttc aaa 221
 Asp Val Ile Trp Asp Thr Leu Gly Asn Lys Gln Phe Cys Ser Phe Lys
 5 10 15 20
 ata aga acc aag act cag agc ttc tgc cga aat gaa tat agc ctg act 269
 Ile Arg Thr Lys Thr Gln Ser Phe Cys Arg Asn Glu Tyr Ser Leu Thr
 25 30 35
 gga ctg tgt aat cgg tca tcc tgt ccc ctg gca aat agt cag tat gcc 317
 Gly Leu Cys Asn Arg Ser Ser Cys Pro Leu Ala Asn Ser Gln Tyr Ala
 40 45 50
 act att aaa gaa gag aaa gga cag tgc tac ttg tat atg aag gtt ata 365
 Thr Ile Lys Glu Glu Lys Gly Gln Cys Tyr Leu Tyr Met Lys Val Ile
 55 60 65
 gaa cga gcg gct ttt cct cgg cgt ctc tgg gaa cgg gtc cgg ctt agt 413
 Glu Arg Ala Ala Phe Pro Arg Arg Leu Trp Glu Arg Val Arg Leu Ser
 70 75 80

aaa aac tat gag aaa gca ctg gag caa ata gat gaa aat ctg att tac	461
Lys Asn Tyr Glu Lys Ala Leu Glu Gln Ile Asp Glu Asn Leu Ile Tyr	
85 90 95 100	
tggtgg ccc cgt ttc att cga cac aaa tgt aag cag aga ttc acc aag atc	509
Trp Pro Arg Phe Ile Arg His Lys Cys Lys Gln Arg Phe Thr Lys Ile	
105 110 115	
acc caa tac cta att cga att aga aaa ctt aca cta aag cga cag agg	557
Thr Gln Tyr Leu Ile Arg Ile Arg Lys Leu Thr Leu Lys Arg Gln Arg	
120 125 130	
aaa ctt gtt cct ttg agt aag aag gtg gag cgt agg gag aaa aga aga	605
Lys Leu Val Pro Leu Ser Lys Lys Val Glu Arg Arg Glu Lys Arg Arg	
135 140 145	
gag gaa aag gca tta ata gct gct cag ctg gac aat gcc att gag aag	653
Glu Glu Lys Ala Leu Ile Ala Ala Gln Leu Asp Asn Ala Ile Glu Lys	
150 155 160	
gaa tta ctg gag aga ctg aaa caa gat acg tat ggc gac atc tac aac	701
Glu Leu Leu Glu Arg Leu Lys Gln Asp Thr Tyr Gly Asp Ile Tyr Asn	
165 170 175 180	
ttc ccc att cat gcc ttc gac aaa gcc ctg gaa caa cag gag gca gag	749
Phe Pro Ile His Ala Phe Asp Lys Ala Leu Glu Gln Gln Glu Ala Glu	
185 190 195	
agt gac tct tca gat act gag gaa aaa gat gat gat gat gat gat gag	797
Ser Asp Ser Ser Asp Thr Glu Glu Lys Asp Asp Asp Asp Asp Asp Glu	
200 205 210	
gaa gat gtg ggg aaa aga gaa ttt gtc gaa gat ggt gag gta gat gag	845
Glu Asp Val Gly Lys Arg Glu Phe Val Glu Asp Gly Glu Val Asp Glu	
215 220 225	
agt gac ata agt gat ttt gag gat atg gat aaa ctg gat gcc agc agt	893
Ser Asp Ile Ser Asp Phe Glu Asp Met Asp Lys Leu Asp Ala Ser Ser	
230 235 240	
gat gaa gat cag gat ggt aaa tcc tcc agt gag gag gag gaa gaa aag	941
Asp Glu Asp Gln Asp Gly Lys Ser Ser Ser Glu Glu Glu Glu Glu Lys	
245 250 255 260	
gcc ctt agt gcg aaa cac aaa ggc aaa atg ccc ttg aga gga cca ctg	989
Ala Leu Ser Ala Lys His Lys Gly Lys Met Pro Leu Arg Gly Pro Leu	
265 270 275	
cag aga aaa cga gcc tat gtg gaa ata gaa tac gag cag gag aca gag	1037
Gln Arg Lys Arg Ala Tyr Val Glu Ile Glu Tyr Glu Gln Glu Thr Glu	
280 285 290	
ccc gtg gcc aaa gcc aaa acc acg tga tttcc ctttcagtca tttataccca	1089
Pro Val Ala Lys Ala Lys Thr Thr *	
295 300	
ggactgaaca tgcagaactg	1109

<210> 281
 <211> 2018
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (36)..(1520)

<220>
 <221> misc_feature
 <222> (1)..(2018)
 <223> n = a,t,c or g

<400> 281
 acagctccca agccacaggc agaagcccca cagag atg gag cag aag gaa ggg 53
 Met Glu Gln Lys Glu Gly
 1 5
 aag ctc tct gag gat ggg acc acc gtc tcc cca gct gcg gac aac cct 101
 Lys Leu Ser Glu Asp Gly Thr Thr Val Ser Pro Ala Ala Asp Asn Pro
 10 15 20
 gag atg tca gga ggt gga gcc cct gca gag gag acc aaa ggc aca gct 149
 Glu Met Ser Gly Gly Gly Ala Pro Ala Glu Glu Thr Lys Gly Thr Ala
 25 30 35
 gga aag gcc atc aat gag ggg cct ccc act gag tca gga aag cag gaa 197
 Gly Lys Ala Ile Asn Glu Gly Pro Pro Thr Glu Ser Gly Lys Gln Glu
 40 45 50
 aag gca cca gcc gag gac ggc atg tca gca gaa ctc cag ggg gaa gca 245
 Lys Ala Pro Ala Glu Asp Gly Met Ser Ala Glu Leu Gln Gly Glu Ala
 55 60 65 70
 aat gga tta gat gag gtc aaa gtg gaa tct cag agg gag gct ggt ggg 293
 Asn Gly Leu Asp Glu Val Lys Val Glu Ser Gln Arg Glu Ala Gly Gly
 75 80 85
 aaa gag gat gct gag gct gaa ctt aaa aag gag gat ggt gag aag gaa 341
 Lys Glu Asp Ala Glu Ala Glu Leu Lys Lys Glu Asp Gly Glu Lys Glu
 90 95 100
 gag acc act gtg ggt tct cag gag atg act ggc agg aaa gaa gag acc 389
 Glu Thr Thr Val Gly Ser Gln Glu Met Thr Gly Arg Lys Glu Glu Thr
 105 110 115
 aaa tct gaa ccc aaa gag gct gag gaa aag gag agc acg ctg gcc tct 437
 Lys Ser Glu Pro Lys Glu Ala Glu Glu Lys Glu Ser Thr Leu Ala Ser
 120 125 130
 gag aag cag aag gct gag gag aaa gag gcc aaa cct gaa tct ggg cag 485
 Glu Lys Gln Lys Ala Glu Glu Lys Glu Ala Lys Pro Glu Ser Gly Gln

135	140	145	150	
aaa gcc gat gcc aat gac aga gac aag cct gaa cct aag gca aca gtt				533
Lys Ala Asp Ala Asn Asp Arg Asp Lys Pro Glu Pro Lys Ala Thr Val	155	160	165	
gag gag gag gac gcc aag aca gcc tct cag gag gag aca ggc cag agg				581
Glu Glu Glu Asp Ala Lys Thr Ala Ser Gln Glu Glu Thr Gly Gln Arg	170	175	180	
aaa gag tgc agc act gaa ccc aag gag aag gct act gat gaa gag gcc				629
Lys Glu Cys Ser Thr Glu Pro Lys Glu Lys Ala Thr Asp Glu Glu Ala	185	190	195	
aag gct gaa tcg cag aag gct gtt gtg gag gat gag gct aag gct gaa				677
Lys Ala Glu Ser Gln Lys Ala Val Val Glu Asp Glu Ala Lys Ala Glu	200	205	210	
ccc aag gag ccc gat ggg aaa gag gag gcc aaa cat ggt gca aaa gag				725
Pro Lys Glu Pro Asp Gly Lys Glu Glu Ala Lys His Gly Ala Lys Glu	215	220	225	230
gag gct gat gca aaa gag gag gcg gag gat gca gag gag gca gag cca				773
Glu Ala Asp Ala Lys Glu Glu Ala Glu Asp Ala Glu Glu Ala Glu Pro	235	240	245	
ggc agt ccc agc gaa gag cag gag cag gac gtg gaa aaa gag cca gag				821
Gly Ser Pro Ser Glu Glu Gln Glu Gln Asp Val Glu Lys Glu Pro Glu	250	255	260	
gga ggg gca ggg gtg att ccc agc tcc cca gag gag tgg cct gag agc				869
Gly Gly Ala Gly Val Ile Pro Ser Ser Pro Glu Glu Trp Pro Glu Ser	265	270	275	
ccc act ggg gag ggg cac aac ctc agc aca gat ggg ctg ggt cca gac				917
Pro Thr Gly Glu Gly His Asn Leu Ser Thr Asp Gly Leu Gly Pro Asp	280	285	290	
tgt gta gct tcc gga cag acc agt cct tca gcc agt gag tct tca ccc				965
Cys Val Ala Ser Gly Gln Thr Ser Pro Ser Ala Ser Glu Ser Ser Pro	295	300	305	310
agc gac gtg ccc cag agt ccc cct gag tcc cct tcc tca ggg gag aag				1013
Ser Asp Val Pro Gln Ser Pro Pro Glu Ser Pro Ser Ser Gly Glu Lys	315	320	325	
aag gag aag gca cca gag cgc agg gta tca gcc cct gct cgg ccc cgg				1061
Lys Glu Lys Ala Pro Glu Arg Arg Val Ser Ala Pro Ala Arg Pro Arg	330	335	340	
ggg ccc ggg gca cag aac cgc aaa gcc atc gtg gac aag ttt ggc ggg				1109
Gly Pro Gly Ala Gln Asn Arg Lys Ala Ile Val Asp Lys Phe Gly Gly	345	350	355	
gca gct tcc ggc ccc acg gcc ttg ttc cgc aac act aag gca gcc ggg				1157
Ala Ala Ser Gly Pro Thr Ala Leu Phe Arg Asn Thr Lys Ala Ala Gly	360	365	370	

gca gcc att ggt ggt gtc aag aac atg ctc ttg gag tgg tgc cga gcc	1205
Ala Ala Ile Gly Gly Val Lys Asn Met Leu Leu Glu Trp Cys Arg Ala	
375 380 385 390	
atg aca aaa aaa tac gag cat gtg gac atc cag aac ttc tcc tcc agc	1253
Met Thr Lys Lys Tyr Glu His Val Asp Ile Gln Asn Phe Ser Ser Ser	
395 400 405	
tgg agc agt ggt atg gcc ttc tgt gcc ctc atc cac aag ttc ttc cct	1301
Trp Ser Ser Gly Met Ala Phe Cys Ala Leu Ile His Lys Phe Phe Pro	
410 415 420	
gac gcc ttt gac tac gca gag ctg gat ccc gca aag cgc cgg cac aac	1349
Asp Ala Phe Asp Tyr Ala Glu Leu Asp Pro Ala Lys Arg Arg His Asn	
425 430 435	
ttc acc ctg gcc ttc tcc aca gca gag aaa ctg gct gac tgt gct cag	1397
Phe Thr Leu Ala Phe Ser Thr Ala Glu Lys Leu Ala Asp Cys Ala Gln	
440 445 450	
ctg ctg gac gtg gat gac atg gtg cgg ttg gct gtg ccc gac tcc aag	1445
Leu Leu Asp Val Asp Asp Met Val Arg Leu Ala Val Pro Asp Ser Lys	
455 460 465 470	
tgc gtc tac aca tac atc cag gaa ctg tac cgc agc ctt gtg cag aaa	1493
Cys Val Tyr Thr Tyr Ile Gln Glu Leu Tyr Arg Ser Leu Val Gln Lys	
475 480 485	
gga ctg gtg aag acc aag aag aag tga ggagg tgactggctc tgtgggcaga	1545
Gly Leu Val Lys Thr Lys Lys Lys *	
490 495	
gatgggcagg gtgcccagct cagcagccac ggcccggggg ttcccttctg ctccatggag	1605
gcaccagagc cagggggctta ggcaaggggtg tgtggcgttg gttttaactg cattaaaagt	1665
acttttgtaa aatcctgtct ggccccctca gtgctctctc ccatacttgg ncccaggaac	1725
ctctgcactc tgggataata aactctggcc cataggggat tctcacctg ctgaggtctc	1785
aataactgcg caaggtgttt gggaaaggac aatggccttg tcccaccact aaccagctgt	1845
gtgacacata cagttaacct ctctgggccc cagtttacag tctgaaaggg gataatgaga	1905
gttccaacct tatgaaggtg ttgcaagagt taaacgagat aatgaaatgg gcaaaaagct	1965
ttgcccagtc ctgccactca agtgttcagt aagtggtcgc caaaaataaa aaa	2018

<210> 282

<211> 706

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (39)..(377)

<400> 282

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                                           Met Thr Leu Val Leu
                                           1          5

tcc atg aat aga ttc tgc gag ccc att gtc tgc gaa gga gct gct gaa      101
Ser Met Asn Arg Phe Cys Glu Pro Ile Val Ser Glu Gly Ala Ala Glu
           10          15          20

att gct ggg tac caa aca cta tgg gag gct gac agc tac gga ggc cca      149
Ile Ala Gly Tyr Gln Thr Leu Trp Glu Ala Asp Ser Tyr Gly Gly Pro
           25          30          35

agc ccc cca ggg cca gca caa gct cct ttg cag gga gac cgg gga gct      197
Ser Pro Pro Gly Pro Ala Gln Ala Pro Leu Gln Gly Asp Arg Gly Ala
           40          45          50

ggt ccc cca ctg gca gct cca ctt ggt gac ttc ctt tct gtg tat cag      245
Gly Pro Pro Leu Ala Ala Pro Leu Gly Asp Phe Leu Ser Val Tyr Gln
           55          60          65

gag cag agc aga gga caa ctt gta gaa gac atg acc att aag aga cat      293
Glu Gln Ser Arg Gly Gln Leu Val Glu Asp Met Thr Ile Lys Arg His
           70          75          80          85

caa ctt cgc aac aaa tat aag aca agg ata caa gga ttc cta tgt gat      341
Gln Leu Arg Asn Lys Tyr Lys Thr Arg Ile Gln Gly Phe Leu Cys Asp
           90          95          100

gca gct agg ttt tta tat cct tct aac aaa tgg tga gcag gagacttttt      391
Ala Ala Arg Phe Leu Tyr Pro Ser Asn Lys Trp *
           105          110

tggaaataat tagttgtgaa attccatttt tctgacagcc ccttaaattt gaagttattt      451

catttgtagt taaggttatc acatccctgc caattttact agattttttc agagacaagc      511

attcagcatg gcattagtaa tgatggttta aactaggtgc agaactgtcc catgaagaga      571

agaatgatat cagtatttaa ataataaaaag aagagacaat gtatggttta tagtgattca      631

ttttaagatt gctgtatttt gattttgtgg tttaaaataa atgcattaag gatcttttaa      691

gttaaaaaaa aaaaaa      706
  
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<210> 283
 <211> 758
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (539)..(697)

<400> 283
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 agtagctgac ctgtgatatc attaggagtt gagctgaaac tacttaaaac tgctctagcc 180
 ccaaccagc tcaactccta atgatatcac aggtcagcta ctcagcttcg ctacctagta 240
 gagaatacag tatgttcatc ctagtgtgaa attttctact ttgatttcca ctgttcttat 300
 acgcattatg tctaagaagc aagaaatgat gacacataat ctaaagaaga aacaatcgat 360
 agaaaaagac cttatggatc acccaagtgt tggaatttag acaaagactt taaaattcca 420
 tgaaaaatth tctttatgth aaagaaaaac gagaggcaga atgattgaga gaatagaaaa 480
 ttgagcaga gaaaaaaaaagt aacaaaatag aaaatctaga actgaaaata tatccgaa 538
 atg aat aaa ttg ttt tat ttg tta ttt att ttt gta gaa aca gga tct 586
 Met Asn Lys Leu Phe Tyr Leu Leu Phe Ile Phe Val Glu Thr Gly Ser
 1 5 10 15
 cat ggt gtt gcc cag gtt ggt ctt gaa ctc ctg agc tca aga gat cct 634
 His Gly Val Ala Gln Val Gly Leu Glu Leu Ser Ser Arg Asp Pro
 20 25 30
 cct gcc tct gcc tcc caa gct gct ggg att aca ggc atg aac cac tgt 682
 Pro Ala Ser Ala Ser Gln Ala Ala Gly Ile Thr Gly Met Asn His Cys
 35 40 45
 gcc cag ctg aaa tga ataaattgga taggcttaac aaaatggata caacaaaatg 737
 Ala Gln Leu Lys *
 50
 gatacaacag aaaaaaaaaa a 758

<210> 284
 <211> 1482
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (939)..(1475)

<400> 284
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 acaatttata tctctcattt catcacacca tctatcagca gacagtcagg ctttaaaaaat 120

caatcccaca ctgactcagt cccacagcaga gatggcctct gacaacagta tccacactgc	180
aggctggaca agggccctat taattttgag actcagccaa atttccttct gaccctaagc	240
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Pro Ser Ser Pro His Leu Trp Met His Gly Gly Leu Gln Ala Gly Leu	
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cca ccg tgg act cag gaa cag gca ggg aag ctg ctg cct cac cag gcg	1097
Pro Pro Trp Thr Gln Glu Gln Ala Gly Lys Leu Leu Pro His Gln Ala	
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aag ggg cca gga ggg gga ggc gga gag gcc cgt cta gcc cct gcg gct	1145
Lys Gly Pro Gly Gly Gly Gly Gly Glu Ala Arg Leu Ala Pro Ala Ala	
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gtc acc gtg gtg cct cct cac tgg cca gtg cgg tcg cgc ctc agc ttc	1193
Val Thr Val Val Pro Pro His Trp Pro Val Arg Ser Arg Leu Ser Phe	
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Val Asn Arg Gly Gly Gly Leu Arg Val Phe Thr Ser Arg Leu Gly Gln	
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Trp Gly Gly Arg Gln Glu Trp Pro Leu Val Phe Gln Thr Ser Gln Gly	
	105 110 115

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Gly Arg Gly Asn Gly Pro Ser Trp Ser Gly Arg Gly Ser Val Phe Arg	
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Trp Met Leu Glu Gly Trp Ala Ala Trp Asp Pro Gly Pro Cys Cys Phe	
135 140 145	
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Pro Glu Asp Ala Leu Ser Gly Ala Ala Gln Val Gly Cys Val Phe Trp	
150 155 160 165	
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Met Glu Leu Leu Leu Leu Glu	
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Thr Phe Gln Trp Asn Leu Cys Leu Pro Thr Ala Ala His Phe Ile Glu	
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Tyr Tyr Leu Ser Glu Ala Val His Glu Thr Asp Leu His Asp Gly Trp	
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Pro Met Ile Cys Leu Glu Lys Thr Lys Leu Tyr Met Ala Lys Tyr Ala	

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Asp Tyr Phe Leu Glu Val Ser Leu Gln Ala Ala Ala Cys Val Ala Ser				
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tcg agg att ata ctt cgt ctt tct cca acg tgg cct aca aga cta cat				652
Ser Arg Ile Ile Leu Arg Leu Ser Pro Thr Trp Pro Thr Arg Leu His				
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cgt ctt act gcc tac tct tgg gat ttc tta gtg cag tgt att gaa cga				700
Arg Leu Thr Ala Tyr Ser Trp Asp Phe Leu Val Gln Cys Ile Glu Arg				
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ctg ttg atc gct cat gat aat gat gtg aaa gaa gca aac aaa cag aga				748
Leu Leu Ile Ala His Asp Asn Asp Val Lys Glu Ala Asn Lys Gln Arg				
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Gly Gln Ala Gly Pro Gln Ser Ala Gln Leu Ser Val Phe Gln Thr Ala				
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Ser Gln Pro Ser Arg Pro Val His Phe Gln Gln Pro Gln Tyr Leu His				
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cag aca cat cag acc tca ctg cag tat cgc cat cct acg tca gaa caa				892
Gln Thr His Gln Thr Ser Leu Gln Tyr Arg His Pro Thr Ser Glu Gln				
	155	160	165	
cca agc tgt cag cag att gta tcg acc aca cac acc tca tct tac aca				940
Pro Ser Cys Gln Gln Ile Val Ser Thr Thr His Thr Ser Ser Tyr Thr				
	170	175	180	
cta cag aca tgt cct gct ggc ttc caa act agt gtt cag ggc ctt ggg				988
Leu Gln Thr Cys Pro Ala Gly Phe Gln Thr Ser Val Gln Gly Leu Gly				
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cac atg cag act ggt gtt ggg atg tca ctg gca ata cca gta gaa gtt				1036
His Met Gln Thr Gly Val Gly Met Ser Leu Ala Ile Pro Val Glu Val				
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Lys Pro Cys Leu Ser Val Ser Tyr Asn Arg Ser Tyr Gln Ile Asn Glu				
	220	225	230	
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His Tyr Pro Cys Ile Thr Pro Cys Phe Glu Arg *				
	235	240		
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gaagagccca ggtccctgcc ccagttctac cacagctctc atgccacag ccctgtctgt 180
ctggacacat tactaggcac agactgctga cagggg atg tcc tgg gcg gtt gac 234
Met Ser Trp Ala Val Asp
1 5

ctg cct gtg tgt caa agg aca cct cac tgc agg gtc caa gac aga gtg 282
Leu Pro Val Cys Gln Arg Thr Pro His Cys Arg Val Gln Asp Arg Val
10 15 20

ctc cac tgt ggc ttc ctg gga agc ccg ctg gtg gga gct cct ggg agc 330
Leu His Cys Gly Phe Leu Gly Ser Pro Leu Val Gly Ala Pro Gly Ser
25 30 35

agg aga cag ctg tgc tct ccc cac tcc tcc ctc cgg cct cag cac cca 378
Arg Arg Gln Leu Cys Ser Pro His Ser Ser Leu Arg Pro Gln His Pro
40 45 50

cag gtg gcc tct gct ctc ttg gag gcg aag ctg ctc ccc tct cct cca 426
Gln Val Ala Ser Ala Leu Leu Glu Ala Lys Leu Leu Pro Ser Pro Pro
55 60 65 70

acc tca ttc tct gcc tgc ttc atc cgg ccc cac aca cac acc ggt aat 474
Thr Ser Phe Ser Ala Cys Phe Ile Arg Pro His Thr His Thr Gly Asn

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Thr	Gly	Arg	Ala	Asp	Arg	Ser	Leu	Arg	Gly	Lys	Pro	Met	Glu	His	Val	
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Ser	Ser	Pro	Cys	Asp	Ser	Asn	Ser	Ser	Ser	Leu	Pro	Arg	Gly	Asp	Val	
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ttg	ggc	agt	tcc	aga	cct	cac	agg	agg	agg	cca	tgt	gtg	caa	caa	agc	599
Leu	Gly	Ser	Ser	Arg	Pro	His	Arg	Arg	Arg	Pro	Cys	Val	Gln	Gln	Ser	
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ctg	tca	agt	tcg	ttc	act	tgt	gaa	aag	gac	ccc	gag	tgc	aaa	gtg	gac	647
Leu	Ser	Ser	Ser	Phe	Thr	Cys	Glu	Lys	Asp	Pro	Glu	Cys	Lys	Val	Asp	
				165					170					175		
cac	aag	aag	ggg	ctc	agg	aaa	agt	gaa	aac	cca	aga	ggc	ccg	ttg	gtc	695
His	Lys	Lys	Gly	Leu	Arg	Lys	Ser	Glu	Asn	Pro	Arg	Gly	Pro	Leu	Val	
			180					185					190			
ctc	cca	gct	gga	ggg	ggg	gcc	caa	gat	gag	agt	ggg	tcc	aga	atc	cac	743
Leu	Pro	Ala	Gly	Gly	Gly	Ala	Gln	Asp	Glu	Ser	Gly	Ser	Arg	Ile	His	
		195					200						205			
cac	aaa	aat	tgg	act	ctt	gca	agt	aag	agg	gga	aga	aac	tca	gcg	cag	791
His	Lys	Asn	Trp	Thr	Leu	Ala	Ser	Lys	Arg	Gly	Arg	Asn	Ser	Ala	Gln	
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aag	gct	agc	ttg	tgc	ctg	aat	gga	tct	tcc	ctt	tca	gag	gac	gac	acg	839
Lys	Ala	Ser	Leu	Cys	Leu	Asn	Gly	Ser	Ser	Leu	Ser	Glu	Asp	Asp	Thr	
		225			230					235					240	
gag	aga	gac	atg	ggg	agc	aaa	gga	ggc	agc	tgg	gca	gcc	ccg	tcc	ttg	887
Glu	Arg	Asp	Met	Gly	Ser	Lys	Gly	Gly	Ser	Trp	Ala	Ala	Pro	Ser	Leu	
				245					250					255		
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Pro	Ser	Gly	Val	Arg	Glu	Asp	Asp	Pro	Cys	Ala	Asn	Ala	Glu	Gly	His	
			260					265					270			
gac	ccc	ggg	ctg	ccg	ttg	ggc	agc	ctc	act	gcg	ccc	cca	gcc	cct	gag	983
Asp	Pro	Gly	Leu	Pro	Leu	Gly	Ser	Leu	Thr	Ala	Pro	Pro	Ala	Pro	Glu	
		275					280					285				
ccc	tcg	gcc	tgc	tca	gag	cct	gga	gaa	tgc	cct	gcg	aaa	aag	agg	ccg	1031
Pro	Ser	Ala	Cys	Ser	Glu	Pro	Gly	Glu	Cys	Pro	Ala	Lys	Lys	Arg	Pro	
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cgc	ctg	gat	ggc	agc	caa	agg	ccg	cct	gcc	gtg	cag	ctg	gag	ccc	atg	1079
Arg	Leu	Asp	Gly	Ser	Gln	Arg	Pro	Pro	Ala	Val	Gln	Leu	Glu	Pro	Met	
		305			310					315					320	
gca	gca	ggg	gcc	gca	cca	tcc	ccc	ggg	ccg	ggg	cca	ggg	ccc	aga	gag	1127
Ala	Ala	Gly	Ala	Ala	Pro	Ser	Pro	Gly	Pro	Gly	Pro	Gly	Pro	Arg	Glu	
				325					330					335		
tct	gtg	acc	ccg	cgc	agc	acc	gcc	agg	ctg	ggc	ccg	cct	ccc	tcc	cac	1175
Ser	Val	Thr	Pro	Arg	Ser	Thr	Ala	Arg	Leu	Gly	Pro	Pro	Pro	Ser	His	

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Ala Ser Ala Asp Ala Thr Arg Cys Leu Pro Cys Pro Asp Ser Gln Lys			
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Leu Glu Lys Glu Cys Gln Ser Ser Glu Glu Ser Met Gly Ser Asn Ser			
370	375	380	
atg cgt tct atc ctg gag gaa gac gag gaa gac gag gag cca cca aga			1319
Met Arg Ser Ile Leu Glu Glu Asp Glu Glu Asp Glu Glu Pro Pro Arg			
385	390	395	400
gtc ctt tta tac cac gaa cca cgt tcg ttt gaa gta gga atg cta gtc			1367
Val Leu Leu Tyr His Glu Pro Arg Ser Phe Glu Val Gly Met Leu Val			
405	410	415	
tgg cat aaa cat aaa aaa tac ccc ttc tgg cca gca gtg gtc aaa agc			1415
Trp His Lys His Lys Lys Tyr Pro Phe Trp Pro Ala Val Val Lys Ser			
420	425	430	
gtc agg cag aga gat aag aaa gca agt gtg cta tac atc gaa gga cac			1463
Val Arg Gln Arg Asp Lys Lys Ala Ser Val Leu Tyr Ile Glu Gly His			
435	440	445	
atg aac ccg aaa atg aaa ggt ttc aca gtg tct ctt aaa agt tta aag			1511
Met Asn Pro Lys Met Lys Gly Phe Thr Val Ser Leu Lys Ser Leu Lys			
450	455	460	
cac ttt gat tgt aaa gag aaa cag acg ctt ctg aat caa gcc agg gag			1559
His Phe Asp Cys Lys Glu Lys Gln Thr Leu Leu Asn Gln Ala Arg Glu			
465	470	475	480
gac ttc aac cag gac atc ggc tgg tgt gct ccc tca tca ccg act aca			1607
Asp Phe Asn Gln Asp Ile Gly Trp Cys Ala Pro Ser Ser Pro Thr Thr			
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ggg tcc ggt tag			1619
Gly Ser Gly *			
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gtaagggaca ccaaggaggt tataatggac ttaaccaatg tttgaaaatt accacaagca 360
aaatatttca atgtaataaa tatgtaaaag tc atg cat aaa ttt tca aat tca 413
Met His Lys Phe Ser Asn Ser
1 5
aat aga cac aag ata aga cat act gaa aat aaa cat ttc aga tgt aaa 461
Asn Arg His Lys Ile Arg His Thr Glu Asn Lys His Phe Arg Cys Lys
10 15 20
gaa tgt gac aaa tca ctt tgc atg ctt tca cgc cta act caa cat aaa 509
Glu Cys Asp Lys Ser Leu Cys Met Leu Ser Arg Leu Thr Gln His Lys
25 30 35
aaa att cat act aga gag aat ttc tac aaa tgt gaa gag tgt gga aaa 557
Lys Ile His Thr Arg Glu Asn Phe Tyr Lys Cys Glu Glu Cys Gly Lys
40 45 50 55
acc ttt aac tgg tcc aca aac ctt tct aaa cct aag aaa att cat act 605
Thr Phe Asn Trp Ser Thr Asn Leu Ser Lys Pro Lys Lys Ile His Thr
60 65 70
gga gaa aaa ccc tac aaa tgt gaa gta tgt gga aaa gcc ttt cac caa 653
Gly Glu Lys Pro Tyr Lys Cys Glu Val Cys Gly Lys Ala Phe His Gln
75 80 85
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Ser Ser Ile Leu Thr Lys His Lys Ile Ile Arg Thr Gly Glu Lys Pro
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tat aaa tgt gca cac tgt ggc aaa gcc ttt aaa cag tcc tca cac ctt 749
Tyr Lys Cys Ala His Cys Gly Lys Ala Phe Lys Gln Ser Ser His Leu
105 110 115
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Thr Arg His Lys Ile Ile His Thr Glu Glu Lys Pro Tyr Lys Cys Glu
120 125 130 135
caa tgt ggc aag gtc ttt aag cag tcc cca acc ctt act aaa cat cag 845
Gln Cys Gly Lys Val Phe Lys Gln Ser Pro Thr Leu Thr Lys His Gln
140 145 150
ata att tat act gga ggt cga cgc gac cgc gaa ttc gga tcc tcg aga 893
Ile Ile Tyr Thr Gly Gly Arg Arg Asp Arg Glu Phe Gly Ser Ser Arg
155 160 165
gat ctc ttt ttt tgg gtt tgg tgg ggt atc ttc gtc atg taa tagggcg 942
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gcacg      atg gcc tcg tct cag ggg aaa aac gag ctg aaa tta gcc gac      167
      Met Ala Ser Ser Gln Gly Lys Asn Glu Leu Lys Leu Ala Asp
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tgg atg gca act ctg ccg gag agc atg cac agc atc ccc ctc acc aat      215
Trp Met Ala Thr Leu Pro Glu Ser Met His Ser Ile Pro Leu Thr Asn
      15              20              25              30

tta gcc att cca ggg tct cat gat tcc ttc agc ttc tac att gat gaa      263
Leu Ala Ile Pro Gly Ser His Asp Ser Phe Ser Phe Tyr Ile Asp Glu
            35              40              45

gcc tct cca gta ggt cct gag cag cca gaa act gtc cag aat ttt gtc      311
Ala Ser Pro Val Gly Pro Glu Gln Pro Glu Thr Val Gln Asn Phe Val
            50              55              60

tct gtg ttt gga act gtg gcc aaa aag ctc atg cgg aaa tgg tta gcc      359
Ser Val Phe Gly Thr Val Ala Lys Lys Leu Met Arg Lys Trp Leu Ala
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act cag aca atg aat ttt act ggc cag cta gga gct gga att cgt tat      407
Thr Gln Thr Met Asn Phe Thr Gly Gln Leu Gly Ala Gly Ile Arg Tyr
            80              85              90

ttt gat ctt cga att tcc acc aag ccc aga gac ccc gac aat gaa ctc      455
Phe Asp Leu Arg Ile Ser Thr Lys Pro Arg Asp Pro Asp Asn Glu Leu
            95              100              105              110

tat ttt gct cat ggt ttg ttc agt gcc aaa gtc aat gaa ggc ctt gag      503
Tyr Phe Ala His Gly Leu Phe Ser Ala Lys Val Asn Glu Gly Leu Glu
            115              120              125

gag atc aat gca ttc ctc aca gat cac cat aag gag gta gtg ttc ttg      551
Glu Ile Asn Ala Phe Leu Thr Asp His His Lys Glu Val Val Phe Leu
            130              135              140

gac ttc aac cac ttc tat ggg atg cag aaa tat cac cat gaa aaa ctg      599
Asp Phe Asn His Phe Tyr Gly Met Gln Lys Tyr His His Glu Lys Leu
            145              150              155

gtc caa atg ctg aaa gac atc tat gga aat aaa atg tgc cca gcg att      647
Val Gln Met Leu Lys Asp Ile Tyr Gly Asn Lys Met Cys Pro Ala Ile
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160	165	170	
ttt gcc cag gaa gtt agt tta aag tac ctg tgg gag aag gac tat caa			695
Phe Ala Gln Glu Val Ser Leu Lys Tyr Leu Trp Glu Lys Asp Tyr Gln			
175	180	185	190
gtg ctg gtc ttc tac cat agt cca gtg gct ctg gaa gtg ccc ttt ctc			743
Val Leu Val Phe Tyr His Ser Pro Val Ala Leu Glu Val Pro Phe Leu			
	195	200	205
tgg cct ggg cag atg atg cca gca ccc tgg gcc aac acc aca gac ccc			791
Trp Pro Gly Gln Met Met Pro Ala Pro Trp Ala Asn Thr Thr Asp Pro			
	210	215	220
gag aaa ctg atc cag ttt ctt caa gca tcc atc act gag aga aga aag			839
Glu Lys Leu Ile Gln Phe Leu Gln Ala Ser Ile Thr Glu Arg Arg Lys			
	225	230	235
aag gga tcg ttt ttt ata tct cag gtg gtg ctg acc ccc aaa gct agc			887
Lys Gly Ser Phe Phe Ile Ser Gln Val Val Leu Thr Pro Lys Ala Ser			
	240	245	250
act gtg gtc aaa ggg gtg gca agt ggc ctc aga gaa aca atc aca gaa			935
Thr Val Val Lys Gly Val Ala Ser Gly Leu Arg Glu Thr Ile Thr Glu			
	255	260	265
aga gct ctt cct gcc atg atg cag tgg gtc cgc acg cag aag cca gga			983
Arg Ala Leu Pro Ala Met Met Gln Trp Val Arg Thr Gln Lys Pro Gly			
	275	280	285
gag agt ggc atc aat att gtc act gcc gat ttt gta gaa ctt ggt gac			1031
Glu Ser Gly Ile Asn Ile Val Thr Ala Asp Phe Val Glu Leu Gly Asp			
	290	295	300
ttt atc agc act gtc ata aag ctc aac tat gtc ttt gat gaa gga gaa			1079
Phe Ile Ser Thr Val Ile Lys Leu Asn Tyr Val Phe Asp Glu Gly Glu			
	305	310	315
gcc aac act tga tag cactacttgg agtttccatg aataagatgg agaaaagctca			1134
Ala Asn Thr *			
	320		
ttgtattagg gcatactatc tgtaaact ctgatcttcc tattccactg agtctctgaa			1194
gggaataggg ctggtagtgg gtgggaaaag gggaaaaact gtttcttcag tgattacaat			1254
catactcttc attactataa atatttcatt tcccatttga tgagcaaaaat ctacttctag			1314
tgtttaggaat aaaaaaaaaa aa			1336

<210> 291
 <211> 3764
 <212> DNA
 <213> Homo sapiens

aag ttg aag cta ttg agc ctc agc cag tca ttc tca tcc act gca ccc Lys Leu Lys Leu Leu Ser Leu Ser Gln Ser Phe Ser Ser Thr Ala Pro 185 190 195 200	747
tct gac aca gac ctc ggg gag agc tta ggg gcc aac gtg gcc acc aca Ser Asp Thr Asp Leu Gly Glu Ser Leu Gly Ala Asn Val Ala Thr Thr 205 210 215	795
gac tcg gat gag aga gat gat gca tct gtg tgc agt gga ggt gac tcc Asp Ser Asp Glu Arg Asp Asp Ala Ser Val Cys Ser Gly Gly Asp Ser 220 225 230	843
act gat gac ggt ggc tac agg agc agc atg tgg gac cag ggc gac atc Thr Asp Asp Gly Gly Tyr Arg Ser Ser Met Trp Asp Gln Gly Asp Ile 235 240 245	891
ctg gag tct ggg tca ggc act tcc ttg gag gag gca ttg gag gcc cca Leu Glu Ser Gly Ser Gly Thr Ser Leu Glu Glu Ala Leu Glu Ala Pro 250 255 260	939
gcc aca gac ctg gcc agg cct gag ttc tgt tac gag gct gag agc cct Ala Thr Asp Leu Ala Arg Pro Glu Phe Cys Tyr Glu Ala Glu Ser Pro 265 270 275 280	987
gat gag gcc gcc ctg gtg cac gct gcc cat gcc tac agc ttc aca cta Asp Glu Ala Ala Leu Val His Ala Ala His Ala Tyr Ser Phe Thr Leu 285 290 295	1035
gtg tcc cgg aca cct gag cag gtg act gtg cgc ctg ccc cag ggc acc Val Ser Arg Thr Pro Glu Gln Val Thr Val Arg Leu Pro Gln Gly Thr 300 305 310	1083
tgc ctc acc ttc agc ctc ctc tgc acc ctg ggc ttt gac tct gtc agg Cys Leu Thr Phe Ser Leu Leu Cys Thr Leu Gly Phe Asp Ser Val Arg 315 320 325	1131
aag aga atg tct gtg gtt gtg agg cac cca ctg act ggc gag att gtt Lys Arg Met Ser Val Val Val Arg His Pro Leu Thr Gly Glu Ile Val 330 335 340	1179
gtc tac acc aag ggt gct gac tcg gtc atc atg gac ctg ctg gaa gac Val Tyr Thr Lys Gly Ala Asp Ser Val Ile Met Asp Leu Leu Glu Asp 345 350 355 360	1227
cca gcc tgc gta cct gac att aat atg gaa aag aag ctg aga aaa atc Pro Ala Cys Val Pro Asp Ile Asn Met Glu Lys Lys Leu Arg Lys Ile 365 370 375	1275
cga gcc cgg acc caa aag cat cta gac ttg tat gca aga gat ggc ctg Arg Ala Arg Thr Gln Lys His Leu Asp Leu Tyr Ala Arg Asp Gly Leu 380 385 390	1323
cgc aca cta tgc att gcc aag aag gtt gta agc gaa gag gac ttc cgg Arg Thr Leu Cys Ile Ala Lys Lys Val Val Ser Glu Glu Asp Phe Arg 395 400 405	1371

aga tgg gcc agt ttc cgg cgt gag gct gag gca tcc ctc gac aac cga	1419
Arg Trp Ala Ser Phe Arg Arg Glu Ala Glu Ala Ser Leu Asp Asn Arg	
410 415 420	
gat gag ctt ctc atg gaa act gca cag cat ctg gag aat caa ctc acc	1467
Asp Glu Leu Leu Met Glu Thr Ala Gln His Leu Glu Asn Gln Leu Thr	
425 430 435 440	
tta ctt gga gcc act ggg atc gaa gac cgg ctg cag gaa gga gtt cca	1515
Leu Leu Gly Ala Thr Gly Ile Glu Asp Arg Leu Gln Glu Gly Val Pro	
445 450 455	
gat acg att gcc act ctg cgg gag gct ggg atc cag ctc tgg gtc ctg	1563
Asp Thr Ile Ala Thr Leu Arg Glu Ala Gly Ile Gln Leu Trp Val Leu	
460 465 470	
act gga gat aag cag gag aca gcg gtc aac att gcc cat tcc tgc aga	1611
Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Ala His Ser Cys Arg	
475 480 485	
ctg tta aat cag acc gac act gtt tat acc atc aat aca gag aat cag	1659
Leu Leu Asn Gln Thr Asp Thr Val Tyr Thr Ile Asn Thr Glu Asn Gln	
490 495 500	
gag acc tgt gaa tcc atc ctc aat tgt gca ttg gaa gag cta aag caa	1707
Glu Thr Cys Glu Ser Ile Leu Asn Cys Ala Leu Glu Glu Leu Lys Gln	
505 510 515 520	
ttt cgt gaa cta cag aag cca gac cgc aag ctc ttt gga ttc cgc tta	1755
Phe Arg Glu Leu Gln Lys Pro Asp Arg Lys Leu Phe Gly Phe Arg Leu	
525 530 535	
cct tcc aag aca cca tcc atc acc tca gaa gct gtg gtt cca gaa gct	1803
Pro Ser Lys Thr Pro Ser Ile Thr Ser Glu Ala Val Val Pro Glu Ala	
540 545 550	
gga ttg gtc atc gat ggg aag aca ttg aat gcc atc ttc cag gga aag	1851
Gly Leu Val Ile Asp Gly Lys Thr Leu Asn Ala Ile Phe Gln Gly Lys	
555 560 565	
cta gag aag aag ttt ctg gaa ttg acc cag tat tgt cgg tcc gtc ctg	1899
Leu Glu Lys Lys Phe Leu Glu Leu Thr Gln Tyr Cys Arg Ser Val Leu	
570 575 580	
tgc tgc cgc tcc acg cca ctc cag aag agt atg ata gtc aag ctg gtg	1947
Cys Cys Arg Ser Thr Pro Leu Gln Lys Ser Met Ile Val Lys Leu Val	
585 590 595 600	
cga gac aag ttg cgc gtc atg acc ctt tcc ata ggt gat gga gca aat	1995
Arg Asp Lys Leu Arg Val Met Thr Leu Ser Ile Gly Asp Gly Ala Asn	
605 610 615	
gat gta agc atg att caa gct gct gat att gga att gga ata tct gga	2043
Asp Val Ser Met Ile Gln Ala Ala Asp Ile Gly Ile Gly Ile Ser Gly	
620 625 630	
cag gaa ggc atg cag gct gtc atg tcc agc gac ttt gcc atc acc cgc	2091

Gln	Glu	Gly	Met	Gln	Ala	Val	Met	Ser	Ser	Asp	Phe	Ala	Ile	Thr	Arg	
		635					640					645				
ttt	aag	cat	ctc	aag	aag	ttg	ctg	ctc	gtg	cat	ggc	cac	tgg	tgt	tac	2139
Phe	Lys	His	Leu	Lys	Lys	Leu	Leu	Leu	Val	His	Gly	His	Trp	Cys	Tyr	
	650					655					660					
tcg	cgc	ctg	gcc	agg	atg	gtg	gtg	tac	tac	ctc	tac	aag	aac	gtg	tgc	2187
Ser	Arg	Leu	Ala	Arg	Met	Val	Val	Tyr	Tyr	Leu	Tyr	Lys	Asn	Val	Cys	
	665				670					675					680	
tac	gtc	aac	ctg	ctc	ttc	tgg	tat	cag	ttc	ttc	tgt	ggc	ttc	tcc	agc	2235
Tyr	Val	Asn	Leu	Leu	Phe	Trp	Tyr	Gln	Phe	Phe	Cys	Gly	Phe	Ser	Ser	
				685					690					695		
tcc	acc	atg	att	gat	tac	tgg	cag	atg	ata	ttc	ttc	aat	ctc	ttc	ttt	2283
Ser	Thr	Met	Ile	Asp	Tyr	Trp	Gln	Met	Ile	Phe	Phe	Asn	Leu	Phe	Phe	
		700						705					710			
acc	tcc	ttg	cct	cct	ctt	gtc	ttt	gga	gtc	ctt	gac	aaa	gac	atc	tct	2331
Thr	Ser	Leu	Pro	Pro	Leu	Val	Phe	Gly	Val	Leu	Asp	Lys	Asp	Ile	Ser	
		715					720					725				
gca	gaa	aca	ctc	ctg	gca	ttg	cct	gag	cta	tac	aag	agt	ggc	cag	aac	2379
Ala	Glu	Thr	Leu	Leu	Ala	Leu	Pro	Glu	Leu	Tyr	Lys	Ser	Gly	Gln	Asn	
	730					735					740					
tct	gag	tgc	tat	aac	ctg	tcg	act	ttc	tgg	att	tct	atg	gtg	gat	gca	2427
Ser	Glu	Cys	Tyr	Asn	Leu	Ser	Thr	Phe	Trp	Ile	Ser	Met	Val	Asp	Ala	
	745				750					755					760	
ttc	tac	cag	agc	ctc	atc	tgt	ttc	ttt	atc	cct	tac	ctg	gcc	tat	aag	2475
Phe	Tyr	Gln	Ser	Leu	Ile	Cys	Phe	Phe	Ile	Pro	Tyr	Leu	Ala	Tyr	Lys	
				765					770					775		
ggc	tct	gat	ata	gat	gtc	ttt	acc	ttt	ggg	aca	cca	atc	aac	acc	atc	2523
Gly	Ser	Asp	Ile	Asp	Val	Phe	Thr	Phe	Gly	Thr	Pro	Ile	Asn	Thr	Ile	
		780						785					790			
tcc	ctc	acc	aca	atc	ctt	ttg	cac	cag	gca	atg	gaa	atg	aag	aca	tgg	2571
Ser	Leu	Thr	Thr	Ile	Leu	Leu	His	Gln	Ala	Met	Glu	Met	Lys	Thr	Trp	
		795					800					805				
acc	att	ttc	cac	gga	gtc	gtg	ctc	ctc	ggc	agc	ttc	ctg	atg	tac	ttt	2619
Thr	Ile	Phe	His	Gly	Val	Val	Leu	Leu	Gly	Ser	Phe	Leu	Met	Tyr	Phe	
	810					815					820					
ctg	gta	tcc	ctc	ctg	tac	aat	gcc	acc	tgc	gtc	atc	tgc	aac	agc	ccc	2667
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Ala	Thr	Cys	Val	Ile	Cys	Asn	Ser	Pro	
	825				830					835					840	
acc	aat	ccc	tat	tgg	gtg	atg	gaa	ggc	cag	ctc	tca	aac	ccc	act	ttc	2715
Thr	Asn	Pro	Tyr	Trp	Val	Met	Glu	Gly	Gln	Leu	Ser	Asn	Pro	Thr	Phe	
				845				850					855			
tac	ctc	gtc	tgc	ttt	ctc	aca	cca	gtt	gtt	gct	ctt	ctc	cca	aga	tac	2763
Tyr	Leu	Val	Cys	Phe	Leu	Thr	Pro	Val	Val	Ala	Leu	Leu	Pro	Arg	Tyr	

ttggttctgc tttttgcctg taagccaaag aaaa

3764

<210> 292
<211> 614
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (361)..(462)

<400> 292

gccacaagaa tgtatacttc tagcaagttt tgttatccta taaggcccag tccaacatat 60
aagtagtcag aaagacttat atgaccataa gaagtagcat acatttcttt ctttgcagtg 120
gtccaatggc aatttgttca cctctaattt ttataatcat agtttagggg tgtgggctaaa 180
agcacaaact ctggaactag actgctagat atataatctt gggtagtgctg tttgattgct 240
ctgggtactct gtacctcaat tttcaccagt taaatgcaga tttaggggtgg gtagttgtga 300
ggattaaaat gtatgggtat accttagaaa ggtgccaaat atggctgggt gtgggtggctc 360
atg tct gta atc cca acc cct tgg aag gcc gag gcg ggt ggc tca caa 408
Met Ser Val Ile Pro Thr Pro Trp Lys Ala Glu Ala Gly Gly Ser Gln
1 5 10 15
ggg cag gag atc aag acc act ctg gcc aac acg gtg aaa cac cgt ctc 456
Gly Gln Glu Ile Lys Thr Thr Leu Ala Asn Thr Val Lys His Arg Leu
20 25 30
cac taa aaatacaaaa tacaataaat tacaataata caaagtacaa aaaatacaaa 512
His *
aaatacaaaa tactgaaaat actaaaaatt agccggggcat agtggcacgt gcctatagtc 572
ccagctactt gggaatctgc ggacgcgtgg gtcgacccgg gt 614

<210> 293
<211> 830
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (219)..(467)

<400> 293

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cgcttgcgaa ccggcccgga attcccgggg cgacccacgc gtccggagcc tgcgagctgc      60
cgaagcaggg ttccgagtc attcgaactg ccatctgata cgctcttata aatgaagcag      120
ccgatcatgg cggatgggcc ccggtgcaag aggcgcaaac aagccaatcc caggaggaaa      180
aacgccttgg agtcagaaat gagcactcgg agcgggag      atg ccc tgc tgc tgc      233
                                         Met Pro Cys Cys Cys
                                         1             5

ttg cca ccg gtg cgg ccc gtt tgt aac ttg caa agt ttg ttg ctt ttg      281
Leu Pro Pro Val Arg Pro Val Cys Asn Leu Gln Ser Leu Leu Leu Leu
              10              15              20

ccc ctg att cgg gca gcg ggt cct ggg atg ctc ctg ctt ccc tcc tgc      329
Pro Leu Ile Arg Ala Ala Gly Pro Gly Met Leu Leu Leu Pro Ser Cys
              25              30              35

ctc cca cgg agc ccg gga aga ggg tct gcc tcc cca tcc cgc cac ctt      377
Leu Pro Arg Ser Pro Gly Arg Gly Ser Ala Ser Pro Ser Arg His Leu
              40              45              50

cca gca tca gcc tct gaa aaa tct cac aga gac atg cac gtt gta gca      425
Pro Ala Ser Ala Ser Glu Lys Ser His Arg Asp Met His Val Val Ala
              55              60              65

aaa atc aaa tcc gga aac tgc ttg ttt cag aga aag aaa tga agttgtc      474
Lys Ile Lys Ser Gly Asn Cys Leu Phe Gln Arg Lys Lys *
              70              75              80

ttttaaagaa aaactgaatt aggaggagag aaaaggggaaa taggagaaga aaggaaaagt      534
taaatttgat ttttctccag agtttccact aaagggttgg ggacagtgtg aaggagaagg      594
ggagcttttt acaaatacct ttggtctctg aacttcagtg gcaaagaaca gggatcaagt      654
tgaatgttct cagggctttg gatcctagag gagaacaat cagaagagca gaaatggtta      714
tcctgttta aaataagccc tactcttta ccacttccct aaaggagtgg aggtgctggg      774
agtgatggtt agaggcaatg agggacggag aagttgctcc cgtttcagag atgctt      830

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<210> 294
 <211> 757
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (493)..(735)

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<400> 294
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acgaggcaac ctcgaggaaa ccacccttat aatggccaag aacaggattg acgattacaa      120
tctcagctgg cctgtcatat aaaacatact gtcattgagc ttaagctccg cttgttctga      180
ggtttcacct ccatgtgttt cattgggtgca aaagtggatc tcttagttgg tcaacttaatt      240
ctttcttttt cagaaagata ggatgttcac tgggtatattt ggtcactctt agaaccttcc      300
ttcacattgt tttttatggg acccatgaat ggtagcctt tcttttctat tgtagaagga      360
aataaatagg agtāaaaaga ccattgtagt aaataagttc aaggggaact tgggaccaga      420
aaccactgtt atgtacaaaa aaatggcaaa ttcaataaac tcaaatttaa aataattttt      480
aaattaacag tt      atg ata aat ttt ata ttt tat aca aat aga ttg ctt      528
                    Met Ile Asn Phe Ile Phe Tyr Thr Asn Arg Leu Leu
                    1             5             10

aga atg gtt ctc aag aat tat aag aga aat gaa ctc aca gta caa aaa      576
Arg Met Val Leu Lys Asn Tyr Lys Arg Asn Glu Leu Thr Val Gln Lys
        15             20             25

ttt tat aat tac tat act tgt gtt ttg ttt ggg ggc tgg gaa atg tat      624
Phe Tyr Asn Tyr Tyr Thr Cys Val Leu Phe Gly Gly Trp Glu Met Tyr
        30             35             40

ttt tac att gta gcc aat cat ttt ata ttt gtc aat tta aat ctt atg      672
Phe Tyr Ile Val Ala Asn His Phe Ile Phe Val Asn Leu Asn Leu Met
        45             50             55             60

ggg ctt ttt ttt tta tct ctc ttg atg tca gat ttt ata gtc ttt tta      720
Gly Leu Phe Phe Leu Ser Leu Leu Met Ser Asp Phe Ile Val Phe Leu
        65             70             75

aat aaa tcc att taa ttaaaacgtt aaaaaaaaaa aa      757
Asn Lys Ser Ile *
        80

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<210> 295
<211> 2388
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (125)..(1258)

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<400> 295
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caagcaactg gattgaacac cctaagaaga aagattcaca ctgcaccagg agacatcaga      120
aaga atg aaa act ctg ccg ctg ttt gtg tgc atc tgt gca ctg agt gct      169

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Met	Lys	Thr	Leu	Pro	Leu	Phe	Val	Cys	Ile	Cys	Ala	Leu	Ser	Ala		
1				5					10					15		
tgc	ttc	tcg	ttc	agt	gaa	ggg	cga	gaa	agg	gat	cat	gaa	cta	cgt	cac	217
Cys	Phe	Ser	Phe	Ser	Glu	Gly	Arg	Glu	Arg	Asp	His	Glu	Leu	Arg	His	
				20					25					30		
aga	agg	cat	cat	cac	caa	tca	ccc	aaa	tct	cac	ttt	gaa	tta	cca	cat	265
Arg	Arg	His	His	His	Gln	Ser	Pro	Lys	Ser	His	Phe	Glu	Leu	Pro	His	
				35					40					45		
tat	cct	gga	ctg	cta	gct	cac	cag	aag	ccg	ttc	att	aga	aag	tcc	tat	313
Tyr	Pro	Gly	Leu	Leu	Ala	His	Gln	Lys	Pro	Phe	Ile	Arg	Lys	Ser	Tyr	
		50						55						60		
aaa	tgt	ctg	cac	aaa	cgc	tgt	agg	cct	aag	ctt	cca	cct	tca	cct	aat	361
Lys	Cys	Leu	His	Lys	Arg	Cys	Arg	Pro	Lys	Leu	Pro	Pro	Ser	Pro	Asn	
	65						70					75				
aac	ccc	ccc	aaa	ttc	cca	aat	cct	cac	cag	cca	cct	aaa	cat	cca	gat	409
Asn	Pro	Pro	Lys	Phe	Pro	Asn	Pro	His	Gln	Pro	Pro	Lys	His	Pro	Asp	
	80						85				90				95	
aaa	aat	agc	agt	gtg	gtc	aac	cct	acc	tta	gtg	gct	aca	acc	caa	att	457
Lys	Asn	Ser	Ser	Val	Val	Asn	Pro	Thr	Leu	Val	Ala	Thr	Thr	Gln	Ile	
				100					105					110		
cca	tct	gtg	act	ttc	cca	tca	gct	tcc	acc	aaa	att	act	acc	ctt	cca	505
Pro	Ser	Val	Thr	Phe	Pro	Ser	Ala	Ser	Thr	Lys	Ile	Thr	Thr	Leu	Pro	
				115					120					125		
aat	gtg	act	ttt	ctt	ccc	cag	aat	gcc	acc	acc	ata	tct	tca	aga	gaa	553
Asn	Val	Thr	Phe	Leu	Pro	Gln	Asn	Ala	Thr	Thr	Ile	Ser	Ser	Arg	Glu	
		130					135						140			
aat	gtt	aac	aca	agc	tct	tct	gta	gct	aca	tta	gca	cca	gtg	aat	tcc	601
Asn	Val	Asn	Thr	Ser	Ser	Ser	Val	Ala	Thr	Leu	Ala	Pro	Val	Asn	Ser	
		145					150					155				
cca	gct	cca	caa	gac	acc	aca	gct	gcc	cca	ccc	aca	cct	tct	gca	act	649
Pro	Ala	Pro	Gln	Asp	Thr	Thr	Ala	Ala	Pro	Pro	Thr	Pro	Ser	Ala	Thr	
	160					165				170					175	
aca	cca	gct	cca	cca	tct	tcc	tca	gct	cca	cca	gag	acc	aca	gct	gcc	697
Thr	Pro	Ala	Pro	Pro	Ser	Ser	Ser	Ala	Pro	Pro	Glu	Thr	Thr	Ala	Ala	
				180					185					190		
cca	ccc	aca	cct	tct	gca	act	aca	caa	gct	cca	cca	tct	tcc	tca	gct	745
Pro	Pro	Thr	Pro	Ser	Ala	Thr	Thr	Gln	Ala	Pro	Pro	Ser	Ser	Ser	Ala	
			195					200					205			
cca	cca	gag	acc	aca	gct	gcc	cca	ccc	aca	cct	cct	gca	act	aca	caa	793
Pro	Pro	Glu	Thr	Thr	Ala	Ala	Pro	Pro	Thr	Pro	Pro	Ala	Thr	Thr	Gln	
		210					215					220				
gct	cca	cca	tct	tcc	tca	gct	cca	cca	gag	acc	aca	gct	gcc	cca	ccc	841
Ala	Pro	Pro	Ser	Ser	Ser	Ala	Pro	Pro	Glu	Thr	Thr	Ala	Ala	Pro	Pro	

225	230	235	
aca cct cct gca act Thr Pro Pro Ala Thr 240	aca cca gct cca cca Thr Pro Ala Pro 245	tct tcc tca gct cca cca Ser Ser Ser Ala Pro Pro 250 255	889
gag acc aca gct gtc Glu Thr Thr Ala Val 260	cca ccc aca cct tct Pro Pro Thr Pro 265	gca act acc cta gac cca Ala Thr Thr Leu Asp Pro 270	937
tca tcc gcc tca gct Ser Ser Ala Ser Ala 275	cca cca gag acc aca Pro Pro Glu Thr Thr 280	gct gcc cca ccc aca cct Ala Ala Pro Pro Thr Pro 285	985
tct gca act aca cca Ser Ala Thr Thr Pro 290	gct cca ccg tct tcc Ala Pro Ser Ser Pro 295	cca gct cca caa gag acc Ala Pro Gln Glu Thr 300	1033
aca gct gcc cca att Thr Ala Ala Pro Ile 305	acc aca cct aat tct Thr Thr Pro Asn Ser 310	tcc cca act act ctt gca Pro Thr Thr Leu Ala 315	1081
cct gac act tct gaa Pro Asp Thr Ser Glu 320	act tca gct gca ccc Thr Ser Ala Ala Pro 325	aca cac cag act act Thr His Gln Thr Thr 330 335	1129
tgc gtc act act caa Ser Val Thr Thr Gln 340	act act act act aaa Thr Thr Thr Thr Lys 345	caa cca act tca gct cct Gln Pro Thr Ser Ala Pro 350	1177
ggc caa aat aaa att Gly Gln Asn Lys Ile 355	tct cga ttt ctt tta Ser Arg Phe Leu Leu 360	tat atg aag aat cta cta Tyr Met Lys Asn Leu Leu 365	1225
aac aga att att gac Asn Arg Ile Ile Asp 370	gac atg gtg gag caa Asp Met Val Glu Gln 375	tag tatattgt atgttgtaaa *	1276
gtgttctgtc atttacaaga tgtgattcat gagtgcagaa ctaccacctt tcttttagca			1336
ccaatcccaa catgaaatta tattactcag atttaaagca ctatcattaa tctttcaatc			1396
taattattca ccaccacaag acctattaac aagacaaaat gcctctatcc cacaagccag			1456
atgcaggtct ggggttcaaa ataactcttt ggatcctaca gagatagcct actgagggca			1516
gagaaagtcc ttagataaag agagaatatt gtatgggcca tcaaccattt acttttccct			1576
gaatgttaga aactacaaaa ccactacctt gtacccccat caaaatccca cctgaaccat			1636
ctaactctat aaacataaag gggtaaaatt ggaactctcc agatgaacaa agacatctaa			1696
atatctgtag atagaaacat ttatctatct aaatatattg atagacctgt cattgtattg			1756
attaatgaca aaacccttta gataattatc ttccatttta aataaaattt tatttcacaa			1816
atatgagcca agaaagagga aagttgattt gaagtgagga ttagaagtga atgacaataa			1876

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agtctggcag ccaagcacga accaagactg gcactatattt tcttagtgta tataattggt 1936
taaactgcaa ggttgacatt tattgtgttg tgtctaagtt aatttcgatc taatgtacct 1996
gattctagcc tctgtgaaca acaagaatat gtttgtgtat gttcacatgg tgcttataat 2056
atttcactat caattcaatt aattcacata aattccatgt gaaatgtatt caacaatgga 2116
atatttttcta aaacatttag tatacatttg aatgtatttt aaaccatgcc aaactactgc 2176
tttaatgtca agtttgacaga attgtctctg aaaataaaaa ccctgacttt agttgtaaaa 2236
caataaaagt tagctacttg gtatacggag atgttaattt gggatatgga ggcattttta 2296
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aagatttcaa atggcaattt aaaaaaaaaa aa 2388

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<210> 296
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<212> DNA
<213> Homo sapiens

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<222> (175) .. (444)

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agcttggcct ctgaaatgag gagattatag gggggaccac cacaccacgc gcctacaaat 120
aaaattattt cacaagatga agagggtata acggcccatg attcccttgg gaat atg 177
Met
1

caa tgg ttt gtt tcc ata act ctg ctg gta ggg atg gaa ttg aaa ccc 225
Gln Trp Phe Val Ser Ile Thr Leu Leu Val Gly Met Glu Leu Lys Pro
5 10 15

acc aca aaa tat aac aac ctg gaa ccc tgc ctt atc acc ttg ata aaa 273
Thr Thr Lys Tyr Asn Asn Leu Glu Pro Cys Leu Ile Thr Leu Ile Lys
20 25 30

cgg gct gtt agg cta gga tac att att caa gag agc aga gtg gga atg 321
Arg Ala Val Arg Leu Gly Tyr Ile Ile Gln Glu Ser Arg Val Gly Met
35 40 45

aga ttt gta ctc aca cct ttt aag gtt gtc cca ctt tca caa gat gtc 369
Arg Phe Val Leu Thr Pro Phe Lys Val Val Pro Leu Ser Gln Asp Val
50 55 60 65

aaa gtg aca cat cat att ggg cct tca att ctg gcc tta tac caa aat 417

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Lys Val Thr His His Ile Gly Pro Ser Ile Leu Ala Leu Tyr Gln Asn
70 75 80

gtg gat aag cat cca gac tat gct tga caaat acaaataagca tccaatatta 469
Val Asp Lys His Pro Asp Tyr Ala *
85 90

acacagaatt tccatgggtt acaatagcag tggtaatccc aaatcatcct gtgaacgtct 529

cctggaatga ctccatagcc acacagaacc acatatggct tcagatagcc atggccctat 589

ttcacttttg tgctgcacca gctgagacct cagctgtagc aaccctcctc tgtccaccta 649

atgccgttta aagcccagcc cctggatttg tgaaccaaact cacatctact atcacagatg 709

agcatatttt tcaactgcca tatgcaccag gctgaatgaa actccccatc cactcccaaa 769

gtcatctcaa aatgtttatg aatccagaca gtgataaata g 810

<210> 297

<211> 883

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<213> Homo sapiens

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<222> (495)..(833)

<400> 297

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ctccagaacc cccatcctct gggctctttt taggccccta gattggcctg cagctgggag 180

cagagtggca agcatgcagg caggcagttg agaaagagga agtcgaggtg ctattgggtc 240

attctgtggt tatcccaggc tctaccagc cagcggttcc cttgggccag ctcgaaacgc 300

tggccgtagg tcatgggagc tgcaggagct gttagccagg ctaggtgcct gcaggttgaa 360

gaactgagct ctatctggct ctgagcccaa gtcatgtgtc cagccttttg actctggagc 420

tgtggcttca gccaccaaga gcagcagttg atcctggaaa cctgagaacc cagacttctt 480

ctctgccatg gggg atg atc agg agg atg att ttc cca ggc ggc tca gcg 530

Met Ile Arg Arg Met Ile Phe Pro Gly Gly Ser Ala
1 5 10

aga gta tgg agg acc tca gcc tgg att tgg ggg ccc ttc agg gca gcg 578

Arg Val Trp Arg Thr Ser Ala Trp Ile Trp Gly Pro Phe Arg Ala Ala
15 20 25

agt atc tgc agg acc tgg gcc ttg ggg ccc ctt ccc aca gcc agc ctg 626

Ser Ile Cys Arg Thr Trp Ala Leu Gly Pro Leu Pro Thr Ala Ser Leu
 30 35 40

ggg aga ccc cag aca gcc gcc cca ccg gtg aag aac cag gaa gag att 674
 Gly Arg Pro Gln Thr Ala Ala Pro Pro Val Lys Asn Gln Glu Glu Ile
 45 50 55 60

ctc ttt tct cca gct tgg cag ggt ccc aag acc tgt caa ggc ggc gca 722
 Leu Phe Ser Pro Ala Trp Gln Gly Pro Lys Thr Cys Gln Gly Gly Ala
 65 70 75

act ggg aaa ggt cgc gga gct gct cac aga gct ggc gga ggc tca acc 770
 Thr Gly Lys Gly Arg Gly Ala Ala His Arg Ala Gly Gly Gly Ser Thr
 80 85 90

tcg atg cct cag ctg tgg atg agg aac cct gtc tcc ccc gaa cac tgg 818
 Ser Met Pro Gln Leu Trp Met Arg Asn Pro Val Ser Pro Glu His Trp
 95 100 105

cca gcc ttg ctt tga acctgccagg aggagggctg aagacctgga ctcaaggggtg 873
 Pro Ala Leu Leu *
 110

tctctctctggg 883

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 1 5 10

tgg gac gga aac agc caa gta gga att gga gac tac aga att cct aag 98
 Trp Asp Gly Asn Ser Gln Val Gly Ile Gly Asp Tyr Arg Ile Pro Lys
 15 20 25

gcg atg ctc aca ttc ttg aat gga agt aga att cct gtc act gag aaa 146
 Ala Met Leu Thr Phe Leu Asn Gly Ser Arg Ile Pro Val Thr Glu Lys
 30 35 40

gca cct cat aaa gga att att aga gat tca acc tgt aag tac ctt cca 194
 Ala Pro His Lys Gly Ile Ile Arg Asp Ser Thr Cys Lys Tyr Leu Pro
 45 50 55 60

gag tgg cag agc tat cag tgc ttt ggg atg gaa tat gca atg atg gtt 242
 Glu Trp Gln Ser Tyr Gln Cys Phe Gly Met Glu Tyr Ala Met Met Val
 65 70 75

att gaa agt ctg gat cct gac aca gaa act cga aga ctt tcc cca gtg Ile Glu Ser Leu Asp Pro Asp Thr Glu Thr Arg Arg Leu Ser Pro Val 80 85 90	290
gct ata atg ggc aac ggt tat gtt gat ctt att aat ggc cca cag gat Ala Ile Met Gly Asn Gly Tyr Val Asp Leu Ile Asn Gly Pro Gln Asp 95 100 105	338
cat ggc tgg tgt gct gga tat aca tgc cag aga agg ctg tcc ctg ttt His Gly Trp Cys Ala Gly Tyr Thr Cys Gln Arg Arg Leu Ser Leu Phe 110 115 120	386
cac agc att gtg gct ctg aac aaa tct tat gaa gtt tac ttc act ggc His Ser Ile Val Ala Leu Asn Lys Ser Tyr Glu Val Tyr Phe Thr Gly 125 130 135 140	434
acc agt cct cag aat ctt cga ctg atg ttg ctt aat gtt gat cat aac Thr Ser Pro Gln Asn Leu Arg Leu Met Leu Leu Asn Val Asp His Asn 145 150 155	482
aag gct gtt cta gta gga att ttc ttt tcc aca ctt caa cgt ttg gat Lys Ala Val Leu Val Gly Ile Phe Phe Ser Thr Leu Gln Arg Leu Asp 160 165 170	530
gtc tat gtg aac aac tta ttg gtc tgt cca aaa act aca ata tgg aat Val Tyr Val Asn Asn Leu Leu Val Cys Pro Lys Thr Thr Ile Trp Asn 175 180 185	578
gcc cag cag aaa cac tgt gaa ctt aat aac cat ctg tac aaa gac caa Ala Gln Gln Lys His Cys Glu Leu Asn Asn His Leu Tyr Lys Asp Gln 190 195 200	626
ttc ctt cct aac ctg gat tcc act gtc ctt ggt gaa aac tac ttt gat Phe Leu Pro Asn Leu Asp Ser Thr Val Leu Gly Glu Asn Tyr Phe Asp 205 210 215 220	674
gga acc tac cag atg ctt tat ctt ttg gtt aaa gga act ata cct gtt Gly Thr Tyr Gln Met Leu Tyr Leu Leu Val Lys Gly Thr Ile Pro Val 225 230 235	722
gaa att cac act gcc aca gtg ata ttt gtt tct ttc caa tta tct gtt Glu Ile His Thr Ala Thr Val Ile Phe Val Ser Phe Gln Leu Ser Val 240 245 250	770
gca aca gaa gat gac ttt tat acc tct cac aat ctg gtt aaa aat ctt Ala Thr Glu Asp Asp Phe Tyr Thr Ser His Asn Leu Val Lys Asn Leu 255 260 265	818
gcc ttg ttc cta aag ata cca agt gac aaa atc cgt atc agc aaa ata Ala Leu Phe Leu Lys Ile Pro Ser Asp Lys Ile Arg Ile Ser Lys Ile 270 275 280	866
aga ggg aag agt ctg agg agg aag aga tcc atg gga ttc ata att gaa Arg Gly Lys Ser Leu Arg Arg Lys Arg Ser Met Gly Phe Ile Ile Glu 285 290 295 300	914

ata gag att gga gac cct cct att cag ttc ata agc aat ggc acc aca Ile Glu Ile Gly Asp Pro Pro Ile Gln Phe Ile Ser Asn Gly Thr Thr 305 310 315	962
ggt cag atg cag tta tct gaa ctc cag gaa att gct ggt tct ctt gga Gly Gln Met Gln Leu Ser Glu Leu Gln Glu Ile Ala Gly Ser Leu Gly 320 325 330	1010
caa gct gta att tta gga aac atc agt agt atc ctt gga ttt aac att Gln Ala Val Ile Leu Gly Asn Ile Ser Ser Ile Leu Gly Phe Asn Ile 335 340 345	1058
tcg tcc atg tct att act aat ccc ctc ccc agc cca agt gac tct ggg Ser Ser Met Ser Ile Thr Asn Pro Leu Pro Ser Pro Ser Asp Ser Gly 350 355 360	1106
tgg att aat gtg act gcc cag cca gtt gaa agg tct gca ttt cct gtt Trp Ile Asn Val Thr Ala Gln Pro Val Glu Arg Ser Ala Phe Pro Val 365 370 375 380	1154
cat cac gtg gcc ttc gtg tcc tca ctc tta gtg atc act cag ccg gtg His His Val Ala Phe Val Ser Ser Leu Leu Val Ile Thr Gln Pro Val 385 390 395	1202
gca gca cag cca gga cag cca ttt cct cag cag cct tcg gta aag gca Ala Ala Gln Pro Gly Gln Pro Phe Pro Gln Gln Pro Ser Val Lys Ala 400 405 410	1250
aca gat tct gac ggt aac tgt gta tca gtt gga att act gca cta act Thr Asp Ser Asp Gly Asn Cys Val Ser Val Gly Ile Thr Ala Leu Thr 415 420 425	1298
ttg agg gcc ata ctc aag gac tcc aat aat aac caa gtc aat ggc ctt Leu Arg Ala Ile Leu Lys Asp Ser Asn Asn Asn Gln Val Asn Gly Leu 430 435 440	1346
agt gga aat aca aca att ccg ttt agc agc tgt tgg gcc aac tac aca Ser Gly Asn Thr Thr Ile Pro Phe Ser Ser Cys Trp Ala Asn Tyr Thr 445 450 455 460	1394
gac ctt act ccc ctt aga aca gga aaa aat tat aag att gaa ttt ata Asp Leu Thr Pro Leu Arg Thr Gly Lys Asn Tyr Lys Ile Glu Phe Ile 465 470 475	1442
ctg gat aat gtt gtt ggg gta gaa tcc aga act ttc agc ctg ctg gca Leu Asp Asn Val Val Gly Val Glu Ser Arg Thr Phe Ser Leu Leu Ala 480 485 490	1490
gag tct gtc tct agc agt ggc agc agc agc agc agc aac agc aaa gca Glu Ser Val Ser Ser Ser Gly Ser Ser Ser Ser Ser Asn Ser Lys Ala 495 500 505	1538
tca act gtg ggt aca tat gcc cag ata atg act gta gta att agc tgt Ser Thr Val Gly Thr Tyr Ala Gln Ile Met Thr Val Val Ile Ser Cys 510 515 520	1586
ctg gtt gga aga atg tgg ctc ttg gaa ata ttt atg gct gca gtt tca	1634

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573

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<212> DNA
<213> Homo sapiens

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<222> (247)..(1245)

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ggtaagcccg cctcctccct cggccggccc tggggccgtg tccgccgggc aactccagcc	180
gaggcctggg cttctgcctg caggtgtctg cggcgaggcc cctagggtac agcccgattt	240
ggcccc atg gtg ggt ttc ggg gcc aac cgg cgg gct ggc cgc ctg ccc	288
Met Val Gly Phe Gly Ala Asn Arg Arg Ala Gly Arg Leu Pro	
1 5 10	
tct ctc gtg ctg gtg gtg ctg ctg gtg gtg atc gtc gtc ctc gcc ttc	336
Ser Leu Val Leu Val Val Leu Leu Val Val Ile Val Val Leu Ala Phe	
15 20 25 30	
aac tac tgg agc atc tcc tcc cgc cac gtc ctg ctt cag gag gag gtg	384
Asn Tyr Trp Ser Ile Ser Ser Arg His Val Leu Leu Gln Glu Glu Val	
35 40 45	
gcc gag ctg cag ggc cag gtc cag cgc acc gaa gtg gcc cgc ggg cgg	432
Ala Glu Leu Gln Gly Gln Val Gln Arg Thr Glu Val Ala Arg Gly Arg	
50 55 60	
ctg gaa aag cgc aat tcg gac ctc ttg ctg ttg gtg gac acg cac aag	480
Leu Glu Lys Arg Asn Ser Asp Leu Leu Leu Val Asp Thr His Lys	
65 70 75	
aaa cag atc gac cag aag gag gcc gac tac ggc cgc ctc agc agc cgg	528
Lys Gln Ile Asp Gln Lys Glu Ala Asp Tyr Gly Arg Leu Ser Ser Arg	
80 85 90	
ctg cag gcc aga gag ggc ctc ggg aag aga tgc gag gat gac aag gtt	576
Leu Gln Ala Arg Glu Gly Leu Gly Lys Arg Cys Glu Asp Asp Lys Val	
95 100 105 110	
aaa cta cag aac aac ata tcg tat cag atg gca gac ata cat cat tta	624
Lys Leu Gln Asn Asn Ile Ser Tyr Gln Met Ala Asp Ile His His Leu	
115 120 125	
aag gag caa ctt gct gag ctt cgt cag gaa ttt ctt cga caa gaa gac	672

Lys Glu Gln Leu Ala Glu Leu Arg Gln Glu Phe Leu Arg Gln Glu Asp	
130 135 140	
cag ctt cag gac tat agg aag aac aat act tac ctt gtg aag agg tta	720
Gln Leu Gln Asp Tyr Arg Lys Asn Asn Thr Tyr Leu Val Lys Arg Leu	
145 150 155	
gaa tat gaa agt ttt cag tgt gga cag cag atg aag gaa ttg aga gca	768
Glu Tyr Glu Ser Phe Gln Cys Gly Gln Gln Met Lys Glu Leu Arg Ala	
160 165 170	
cag cat gaa gaa aat att aaa aag tta gca gac cag ttt tta gag gaa	816
Gln His Glu Glu Asn Ile Lys Lys Leu Ala Asp Gln Phe Leu Glu Glu	
175 180 185 190	
caa aag caa gag acc caa aag att caa tca aat gat gga aag gaa ttg	864
Gln Lys Gln Glu Thr Gln Lys Ile Gln Ser Asn Asp Gly Lys Glu Leu	
195 200 205	
gat ata aac aat caa gta gta cct aaa aat att cca aaa gta gct gag	912
Asp Ile Asn Asn Gln Val Val Pro Lys Asn Ile Pro Lys Val Ala Glu	
210 215 220	
aat gtt gca gat aag aat gaa gaa ccc tca agc aat cat att cca cat	960
Asn Val Ala Asp Lys Asn Glu Glu Pro Ser Ser Asn His Ile Pro His	
225 230 235	
ggg aaa gaa caa atc aaa aga ggt ggt gat gca ggg atg cct gga ata	1008
Gly Lys Glu Gln Ile Lys Arg Gly Gly Asp Ala Gly Met Pro Gly Ile	
240 245 250	
gaa gag aat gac cta gca aaa gtt gat gat ctt ccc cct gct tta agg	1056
Glu Glu Asn Asp Leu Ala Lys Val Asp Asp Leu Pro Pro Ala Leu Arg	
255 260 265 270	
aag cct cct att tca gtt tct caa cat gaa agt cat caa gca atc tcc	1104
Lys Pro Pro Ile Ser Val Ser Gln His Glu Ser His Gln Ala Ile Ser	
275 280 285	
cat ctt cca act gga caa gct ctc tcc cca aat atg cct cca gat tca	1152
His Leu Pro Thr Gly Gln Ala Leu Ser Pro Asn Met Pro Pro Asp Ser	
290 295 300	
cac att aaa cac aat gga aac ccc ggt act tca aaa aca gaa tcc ttc	1200
His Ile Lys His Asn Gly Asn Pro Gly Thr Ser Lys Thr Glu Ser Phe	
305 310 315	
cag tcc tct tca gcg ttt aat tcc agg ctc aaa ctt gga cag tag aac	1248
Gln Ser Ser Ser Ala Phe Asn Ser Arg Leu Lys Leu Gly Gln *	
320 325 330	
ccagaaattc caaacagatt atactaaagg caggttacca aggacagaag ccggggattc	1308
ccataaaaatt ggcaccaatg tgaacacaga gagctcgtaa actgggtcct ggaccttggc	1368
agcacgcttc accgacgtcc tcaaaaccca gaggacacac tcgaaaacga aaagggggcg	1428

aaccgcaaca cccacggccc ccccgacccg gaagggacga aagacagggt acaccaggac 1488
acacaaaatg gcaaaacaaa ggcaacacgc tccaagaaag aacagccata cacaaaagaa 1548
caaaagcgca cacaccaaac aaccccgcac gaaccaacac cacaccaaga catgtcaaca 1608
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aaaccaccaa cggacaccca ctgcccagcc tgtatcattc ctactagaca 1718

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<213> Homo sapiens

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tgtcagtgac tgaggttcgc tgtgacacag aggggttctc ctggagagct atggcac 177
atg ctc cat att aaa agg caa cat gat gct cgc tcc acc cag agg ccc 225
Met Leu His Ile Lys Arg Gln His Asp Ala Arg Ser Thr Gln Arg Pro
1 5 10 15
cgg tcc ccg cca ttc att ccg ctc ccg gcc gag agt cgc tct agc caa 273
Arg Ser Pro Pro Phe Ile Pro Leu Pro Ala Glu Ser Arg Ser Ser Gln
20 25 30
tca cct tcc agg ctc agg gcg gcc gag gca ggg cct ctg cct ctt cgg 321
Ser Pro Ser Arg Leu Arg Ala Ala Glu Ala Gly Pro Leu Pro Leu Arg
35 40 45
ggg gcc tct ccc tcc ccc tgc ccc tga ttgtg gctgaactgc caccgcttga 373
Gly Ala Ser Pro Ser Pro Cys Pro *
50 55
tagcaaacca cactcggcac aggaaggaga acagcgcccg cggcacgaaa 423

<210> 302
<211> 408
<212> DNA
<213> Homo sapiens

<220>
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<222> (44)..(343)

<400> 302
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 Met Ser Ser Pro
 1

ccg cca aga cgc tcc aac cgc cgc aat cct tgt cca tca ggc atc cag 103
 Pro Pro Arg Arg Ser Asn Arg Arg Asn Pro Cys Pro Ser Gly Ile Gln
 5 10 15 20

gcc aga aac tct ggc tgc ccc cac ctg ccc aat ggt ccc cat caa gta 151
 Ala Arg Asn Ser Gly Cys Pro His Leu Pro Asn Gly Pro His Gln Val
 25 30 35

ggt aac atc ctg ctg att tta act cct gtg cag ccc tca aat gca caa 199
 Gly Asn Ile Leu Leu Ile Leu Thr Pro Val Gln Pro Ser Asn Ala Gln
 40 45 50

ctg cct ccc att cct gca cag tgc ccc agt tca ggc ctt cac cac ctt 247
 Leu Pro Pro Ile Pro Ala Gln Cys Pro Ser Ser Gly Leu His His Leu
 55 60 65

gtt cct ggg cca ctg ccc aag tct ccc ccg act ggt ggc tgg act tct 295
 Val Pro Gly Pro Leu Pro Lys Ser Pro Pro Thr Gly Gly Trp Thr Ser
 70 75 80

aat act ttt cca act ccc cac tca tta aat cca tcc ccc tct cat taa 343
 Asn Thr Phe Pro Thr Pro His Ser Leu Asn Pro Ser Pro Ser His *
 85 90 95 100

ctggtgggaa ttgaggaaaa ctgagttcca gccttgtcat cctcatactc atgacccttc 403
 caggc 408

<210> 303
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 <212> DNA
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<220>
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 <222> (69)..(590)

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ccaaggaa atg cca caa tca ttt tct gca atc aca tta agt aac aca gag 110
 Met Pro Gln Ser Phe Ser Ala Ile Thr Leu Ser Asn Thr Glu
 1 5 10

atg aat aat att aat act aat gcc ccg aga aac aaa ctt cca ata aag 158
 Met Asn Asn Ile Asn Thr Asn Ala Pro Arg Asn Lys Leu Pro Ile Lys
 15 20 25 30

gaa ctt ggt aaa gtt tct aaa cat aaa att gcc act aaa aga aca cca	206
Glu Leu Gly Lys Val Ser Lys His Lys Ile Ala Thr Lys Arg Thr Pro	
35 40 45	
cat aaa gaa gat gag gca atg agc tgt tct gaa aat tgt tcg agt gcc	254
His Lys Glu Asp Glu Ala Met Ser Cys Ser Glu Asn Cys Ser Ser Ala	
50 55 60	
cag ggc gac tca ctt cag gat gag tct caa ggg tct cat tct gag tcc	302
Gln Gly Asp Ser Leu Gln Asp Glu Ser Gln Gly Ser His Ser Glu Ser	
65 70 75	
agc tct aat ccc tcc aat cct gaa act ttg cat gca aag gca act gat	350
Ser Ser Asn Pro Ser Asn Pro Glu Thr Leu His Ala Lys Ala Thr Asp	
80 85 90	
tca gtt cta caa ggt tct gaa gga aac aag gtc aag agg aca tcc tgc	398
Ser Val Leu Gln Gly Ser Glu Gly Asn Lys Val Lys Arg Thr Ser Cys	
95 100 105 110	
atg tat ggg gca aac tgc tat agg aag aat cct gtt cat ttt caa cat	446
Met Tyr Gly Ala Asn Cys Tyr Arg Lys Asn Pro Val His Phe Gln His	
115 120 125	
ttt agc cat cct ggt gat agt gat tat gga ggt gta caa atc gtg ggc	494
Phe Ser His Pro Gly Asp Ser Asp Tyr Gly Gly Val Gln Ile Val Gly	
130 135 140	
caa gat gag act gat gac cgg cct gaa tgt ccc tat gga cca tcc tgt	542
Gln Asp Glu Thr Asp Asp Arg Pro Glu Cys Pro Tyr Gly Pro Ser Cys	
145 150 155	
tat agg ttg gaa gtt cag tgt cca gtt gaa aaa cac caa ctc agc tag	590
Tyr Arg Leu Glu Val Gln Cys Pro Val Glu Lys His Gln Leu Ser *	
160 165 170	
tttcttctg tctgcattac agtatctttac ctgtcttttt atgaaaagag cacgttctag	650
gaaaggatgg aagattctca aagaaacaac tttccccttc taaggcagat gaaaacctgt	710
acatgtacct aacatttttt ccccttttta aaatataaaa tttcacatta catttttctgc	770
tcttcctttt tggaataatt aaatgtaaca cttctttcat aaaaaaaaaa aa	822

<210> 304
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (121)..(309)

<400> 304

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tttgaaagct gattgatagc cgtaccgcac cgcaaaccac gggtcgaccc acgcgtccgc      60
ttcacttcac cttcactact tctgtagtct gatcttgtgt aatagagaac ccagccaact      120
atg aag ttc ctt gac ttt gct ttc atc ttg gct ctc aag gtt tcc atg      168
Met Lys Phe Leu Asp Phe Ala Phe Ile Leu Ala Leu Lys Val Ser Met
  1           5           10          15
att gga gct gat tcc tct gaa gag aaa ttt ttg cgt ata att gta cga      216
Ile Gly Ala Asp Ser Ser Glu Glu Lys Phe Leu Arg Ile Ile Val Arg
          20           25           30
atc ggt tat ggg tat ggc cct tat cat tca gtt tca gaa caa cca cta      264
Ile Gly Tyr Gly Tyr Gly Pro Tyr His Ser Val Ser Glu Gln Pro Leu
          35           40           45
tac cca caa cca tac caa cca caa tac caa caa tat acc ttt taa tat      312
Tyr Pro Gln Pro Tyr Gln Pro Gln Tyr Gln Gln Tyr Thr Phe *
          50           55           60
catcagtaac tgcaggacat gattattgag gcttgattgg ctgatacgac ttctacatcc      372
atattctcat gtttcatacc atatcgact actaccactt tttgaagaat catcatagag      432
ctttgcatat gagaaacact atatg      457

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<220>
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<222> (85) .. (873)

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atgatgaaga ggcagctgca ccgc      atg cgg cag ctg gcc cag acg ggc agc      111
                                Met Arg Gln Leu Ala Gln Thr Gly Ser
                                1           5
ttg gga cgc acc ccg gag acc gct gag ttc ctg ggt gag gac ctg ctg      159
Leu Gly Arg Thr Pro Glu Thr Ala Glu Phe Leu Gly Glu Asp Leu Leu
  10           15           20           25
cag gta gaa cag cgg ctg gag ccg gcc aag cgg gca gcc cac aac atc      207
Gln Val Glu Gln Arg Leu Glu Pro Ala Lys Arg Ala Ala His Asn Ile
          30           35           40
cac aag cgg ctg cag gcc tgt ctg cag ggc cag agc ggg gca gac atg      255
His Lys Arg Leu Gln Ala Cys Leu Gln Gly Gln Ser Gly Ala Asp Met
          45           50           55

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gac aag cgg gtg aag aag ctt ccc ctc atg gct ctg tcc acc acg atg Asp Lys Arg Val Lys Lys Leu Pro Leu Met Ala Leu Ser Thr Thr Met 60 65 70	303
gct gag agc ctc aag gag ctg gac cct gat tcc agc atg ggg aag gcc Ala Glu Ser Leu Lys Glu Leu Asp Pro Asp Ser Ser Met Gly Lys Ala 75 80 85	351
ttg gag atg agc tgt gcc atc cag aat cag ctg gcc cgc atc ctg gcc Leu Glu Met Ser Cys Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu Ala 90 95 100 105	399
gag ttt gag atg acc ctg gag agg gac gtc ctg cag cca ctc agc agg Glu Phe Glu Met Thr Leu Glu Arg Asp Val Leu Gln Pro Leu Ser Arg 110 115 120	447
ctg agt gag gag gag ctg cca gcc atc ctc aaa cac aag aaa agc ctc Leu Ser Glu Glu Glu Leu Pro Ala Ile Leu Lys His Lys Lys Ser Leu 125 130 135	495
cag aag ctc gtg tcc gac tgg aac aca ctc aag agc agg ctc agt cag Gln Lys Leu Val Ser Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser Gln 140 145 150	543
gca acc aag aat tca ggc agc agt caa ggc cta gga ggc agc ccg ggt Ala Thr Lys Asn Ser Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro Gly 155 160 165	591
agt cac agc cat acg acc atg gcc aac aag gtg gag acg ctg aag gag Ser His Ser His Thr Thr Met Ala Asn Lys Val Glu Thr Leu Lys Glu 170 175 180 185	639
gag gag gag gag ctg aag agg aaa gtg gag caa tgc agg gac gag tac Glu Glu Glu Glu Leu Lys Arg Lys Val Glu Gln Cys Arg Asp Glu Tyr 190 195 200	687
ttg gct gac ctg tac cac ttt gtt acc aag gag gac tcc tat gcc aac Leu Ala Asp Leu Tyr His Phe Val Thr Lys Glu Asp Ser Tyr Ala Asn 205 210 215	735
tac ttc att cgt ctc ctg gag att cag gcc gat tac cat cgc agg tca Tyr Phe Ile Arg Leu Leu Glu Ile Gln Ala Asp Tyr His Arg Arg Ser 220 225 230	783
ctg agc tcg ctg gac aca gcc ctg gct gag ctg agg gag aac cac gcc Leu Ser Ser Leu Asp Thr Ala Leu Ala Glu Leu Arg Glu Asn His Gly 235 240 245	831
caa gca ggt ggg gac ata ggc ccg gcg ata cca cac ccc tga ccctgcc Gln Ala Gly Gly Asp Ile Gly Pro Ala Ile Pro His Pro * 250 255 260	880
ctgctcgggg cttattgaga agctcgcact tcacctgaa aggtagcagg aagctgtgga	940
tgggttctga gagctaggct caatctgtga tggagaggca gctctggcta ctgtgtggag	1000
ggtggagtga agcgggcagg actagagcca ggcctgtgag gcagaaggag gcaacggtgg	1060

cctggactag gacagaggca gtggaggcgg gctgattcga gagatgtgac ggatgatttc 1120
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 aaccacactg caagagctgg gccgggagat tgcctgccc atcgaggcct gcgtcatgat 1360
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 cgacccgcac gctgtggcag gtgcctcaa gtctatctg cgggagctgc cagagcctct 1540
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 ccggctgcag gccctccaag aggtgtgcag ccgcctaccc cccgagaacc tcagcaacct 1660
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 atctcgacag cgaagtcgac ccgggaatt 1749

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 <213> Homo sapiens

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 Ala Thr Gly Thr Pro Glu Ser Gln Ala Arg Phe Gly Gln Ser Val Lys
 5 10 15
 ggg ctt ctc acg gag aag gtg acc acc tgt ggt act gac gta atc gcg 153
 Gly Leu Leu Thr Glu Lys Val Thr Thr Cys Gly Thr Asp Val Ile Ala
 20 25 30
 ctc acc aag cag gtg ctg aaa ggc tcc cgg agc tcc gag ctg cta ggt 201
 Leu Thr Lys Gln Val Leu Lys Gly Ser Arg Ser Ser Glu Leu Leu Gly
 35 40 45
 cag gca gct cga aac atg gta ctc cag gaa gat gcc atc ttg cac tca 249
 Gln Ala Ala Arg Asn Met Val Leu Gln Glu Asp Ala Ile Leu His Ser
 50 55 60 65

gaa gat agt tta agg aag atg gca ata ata aca aca cat ctt caa tac 297
 Glu Asp Ser Leu Arg Lys Met Ala Ile Ile Thr Thr His Leu Gln Tyr
 70 75 80
 cag caa gaa gct att cag aag aat gtt gaa cag tca tcg gat cta cag 345
 Gln Gln Glu Ala Ile Gln Lys Asn Val Glu Gln Ser Ser Asp Leu Gln
 85 90 95
 gac cag ttg aat cat ctg ttg aaa tag aatga catgtaagag tgctgtagga 397
 Asp Gln Leu Asn His Leu Leu Lys *
 100 105
 ctccctttgcc taatgctgag gagtaaatac cttacacagc tgtcctctgg gtttggtttt 457
 ctatctttctt ctccaaaagt taagttagaa aagttcttg 496

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 <211> 1438
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 <213> Homo sapiens

<220>
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 <222> (88) .. (840)

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 gttccaggat ccaggtgccc aggggtc atg aag ctg gga ctc ctc tgt gct 111
 Met Lys Leu Gly Leu Leu Cys Ala
 1 5
 ctg ctc tct ctg ctg gca ggg cat ggc tgg gca gac acc cgt gcc atc 159
 Leu Leu Ser Leu Leu Ala Gly His Gly Trp Ala Asp Thr Arg Ala Ile
 10 15 20
 ggg gcc gag gaa tgt cgc ccc aac tcc cag cct tgg cag gcc ggc ctc 207
 Gly Ala Glu Glu Cys Arg Pro Asn Ser Gln Pro Trp Gln Ala Gly Leu
 25 30 35 40
 ttc cac ctt act cgg ctc ttc tgt ggg gcg acc ctc atc agt gac cgc 255
 Phe His Leu Thr Arg Leu Phe Cys Gly Ala Thr Leu Ile Ser Asp Arg
 45 50 55
 tgg ctg ctc aca gct gcc cac tgc cgc aag ccg tat ctg tgg gtc cgc 303
 Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro Tyr Leu Trp Val Arg
 60 65 70
 ctt gga gag cac cac ctc tgg aaa tgg gag ggt ccg gag cag ctg ttc 351
 Leu Gly Glu His His Leu Trp Lys Trp Glu Gly Pro Glu Gln Leu Phe
 75 80 85
 cgg gtt acg gac ttc ttc ccc cac cct ggc ttc aac aag gac ctc agc 399

Arg	Val	Thr	Asp	Phe	Phe	Pro	His	Pro	Gly	Phe	Asn	Lys	Asp	Leu	Ser		
90						95					100						
gcc	aat	gac	cac	aat	gat	gac	atc	atg	ctg	atc	cgc	ctg	ccc	agg	cag	447	
Ala	Asn	Asp	His	Asn	Asp	Asp	Ile	Met	Leu	Ile	Arg	Leu	Pro	Arg	Gln		
105					110					115					120		
gca	cgt	ctg	agt	cct	gct	gtg	cag	ccc	ctc	aac	ctc	agc	cag	acc	tgt	495	
Ala	Arg	Leu	Ser	Pro	Ala	Val	Gln	Pro	Leu	Asn	Leu	Ser	Gln	Thr	Cys		
				125					130						135		
gtc	tcc	cca	ggc	atg	cag	tgt	ctc	atc	tca	ggc	tgg	ggg	gcc	gtg	tcc	543	
Val	Ser	Pro	Gly	Met	Gln	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ala	Val	Ser		
			140					145						150			
agc	ccc	aag	gcg	ctg	ttt	cca	gtc	aca	ctg	cag	tgt	gcc	aac	atc	agc	591	
Ser	Pro	Lys	Ala	Leu	Phe	Pro	Val	Thr	Leu	Gln	Cys	Ala	Asn	Ile	Ser		
		155					160						165				
atc	ctg	gag	aac	aaa	ctc	tgt	cac	tgg	gca	tac	cct	gga	cac	atc	tcg	639	
Ile	Leu	Glu	Asn	Lys	Leu	Cys	His	Trp	Ala	Tyr	Pro	Gly	His	Ile	Ser		
		170				175						180					
gac	agc	atg	ctc	tgt	gcg	ggc	ctg	tgg	gag	ggg	ggc	cga	ggg	tcc	tgc	687	
Asp	Ser	Met	Leu	Cys	Ala	Gly	Leu	Trp	Glu	Gly	Gly	Arg	Gly	Ser	Cys		
185					190					195					200		
cag	ggg	gac	tct	ggg	ggc	ccc	ctg	gtt	tgc	aat	gga	acc	ttg	gca	ggc	735	
Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Thr	Leu	Ala	Gly		
				205					210						215		
gtg	gtg	tct	ggg	ggg	gct	gag	ccc	tgc	tcc	aga	ccc	cgg	cgc	ccc	gca	783	
Val	Val	Ser	Gly	Gly	Ala	Glu	Pro	Cys	Ser	Arg	Pro	Arg	Arg	Pro	Ala		
			220					225						230			
gtc	tac	acc	agc	gta	tgc	cac	tac	ctt	gac	tgg	atc	caa	gaa	atc	atg	831	
Val	Tyr	Thr	Ser	Val	Cys	His	Tyr	Leu	Asp	Trp	Ile	Gln	Glu	Ile	Met		
		235					240					245					
gag	aac	tga	gcccgcg	cgccacgggg	gcaccttgga	agaccaagag	aggccgaagg									887	
Glu	Asn	*															
		250															
gcacggggta	gggggttctc	gtaggggtccc	agcctcaatg	gttcccgcgc	tggaacctcca											947	
gctgccctga	ctcccctctg	gacactaaga	ctccgcccct	gaggctccgc	cccctcacga											1007	
ggtcaagcaa	gacacagtcg	cgccccctcg	gaacggagca	gggacacgcc	cttcagagcc											1067	
cgtctctatg	acgtcaccga	cagccatcac	ctccttcttg	gaacagcaca	gcctgtggct											1127	
ccgccccaaag	gaaccactta	cacaaaatag	ctccgcccct	cggaactttg	cccagtggga											1187	
cttcccctcg	ggactccacc	ccttgtggcc	ccgcctcctt	caccagagat	ctcgcccctc											1247	
gtgatgtcag	gggcgcagta	gctccgcccc	cgtggagctc	gggcgggtgta	gagctcagcc											1307	

ccttgtggcc cgcctcctggg cgtgtgctgg gtttgaatcc tggcggagac ctgggggggaa 1367
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gggaaacctc a 1438

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gccagccctc acctgacttg tctgggtccc tcctggggct aggggatgg atg aga 115
Met Arg
1
agg gct agg ctg gag ctg tca gca gct tct tgg tgc ctg ctg ttt ctc 163
Arg Ala Arg Leu Glu Leu Ser Ala Ala Ser Trp Cys Leu Leu Phe Leu
5 10 15
ttg tct tgt ctg tct tcg gtg tat tgc aat cct gtc ctc tta gca ggc 211
Leu Ser Cys Leu Ser Ser Val Tyr Cys Asn Pro Val Leu Leu Ala Gly
20 25 30
ccc gca gag tca tac ttt ttc tcc ctg gcc ttc cag ctc cct ctc ttc 259
Pro Ala Glu Ser Tyr Phe Phe Ser Leu Ala Phe Gln Leu Pro Leu Phe
35 40 45 50
cac cca gta tgc cca cct ccc tct ccc ttg act acc cca gcc tct gcc 307
His Pro Val Cys Pro Pro Pro Ser Pro Leu Thr Thr Pro Ala Ser Ala
55 60 65
caa tca cgc cct gcc ctc tac cct tca gag gac acc ttg ccg tct gtg 355
Gln Ser Arg Pro Ala Leu Tyr Pro Ser Glu Asp Thr Leu Pro Ser Val
70 75 80
gag ctg gag cta ttc cta tgg tct ctc tgg gtc cac atg acc tta cat 403
Glu Leu Glu Leu Phe Leu Trp Ser Leu Trp Val His Met Thr Leu His
85 90 95
ggc act cct ctc acc ttc tgt cca tcc aac aaa att ctc tgt tcc ttt 451
Gly Thr Pro Leu Thr Phe Cys Pro Ser Asn Lys Ile Leu Cys Ser Phe
100 105 110
gaa gct ctc ttt tca gta agg cct tcc ttg gcc cct aac agg atg gat 499
Glu Ala Leu Phe Ser Val Arg Pro Ser Leu Ala Pro Asn Arg Met Asp
115 120 125 130

cac cct ccc ctg agc cct ggt cat tgc ctc tct gtt atg gcc tct cca	547
His Pro Pro Leu Ser Pro Gly His Cys Leu Ser Val Met Ala Ser Pro	
135 140 145	
ttg gta aac gct ctg ccg atg tgt ttc atc ttc cca cta gat cct tgc	595
Leu Val Asn Ala Leu Pro Met Cys Phe Ile Phe Pro Leu Asp Pro Cys	
150 155 160	
gcc cac gca cgc ggc tga atcatc tttacatccc cagaggccct ggtatgtggt	649
Ala His Ala Arg Gly *	
165	
ggacaggctt gtttctgccg ggcctt	675

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<220>
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cagtcactta ttcccttcat acctgtcagc cgagagcact gactgcgtga tttccagggg	180
cctttacagc tttagagtat aggggctctg tttttgctgc tcccgaattt ccacctccca	240
tcatccacgc atttcacaga tgcactctgaa tgctcacagt gctctatttg tgctcttctg	300
tttgtccctg ttttttatgt ggatgcgtat cgaccgccat gatagactgc aactccctg	360
tgggcaggag ccatgttcat ttcatttttg tgtcccaggc ataatgtagg tgcgctcacc	420
tcactctctcc catatcttga acctgtgaat ctcagtggac tcttttcagc agatgaacct	480
gtataagtct ttcctgtctt gaaaggacag atgggtggcc cccatcctcc actgagcttc	540
ctgttgaact ccctttgcag gtgacgtcaa aatagaagaa gccctcattc accatatcta	600
ctgttaccct cctcctttcc cctctacttc ccatgaccag ttgttcaactg cccctccaca	660
gaacctactt ctgataaatt ccgtgaagaa ttttttattg ccagatccaa attctttggc	720
ctctcacagt gtttgctgtg gcctgattct cctcattctt ggaaactcct ctctctct	778
atg gct ccc atg gga cca gtt gct cct gca gct cct cct gcc cct cac	826
Met Ala Pro Met Gly Pro Val Ala Pro Ala Ala Pro Pro Ala Pro His	
1 5 10 15	
tct gct ctc ctt gga ctc ctc ttt cct ggt att ctc tgc agt tct gtc	874

Ser	Ala	Leu	Leu	Gly	Leu	Leu	Phe	Pro	Gly	Ile	Leu	Cys	Ser	Ser	Val	
		20						25					30			
ctt	cgc	tct	cag	ctc	ttt	gca	ccc	ttc	ttt	ccc	tcg	ctg	aca	gct	tcg	922
Leu	Arg	Ser	Gln	Leu	Phe	Ala	Pro	Phe	Phe	Pro	Ser	Leu	Thr	Ala	Ser	
		35					40					45				
cgc	ata	cct	gtg	gct	tca	ctg	tca	cgc	taa	g	gaacattctc	tgtggccctg				973
Arg	Ile	Pro	Val	Ala	Ser	Leu	Ser	Arg	*							
		50					55									
gcccgtctct	cgagcctgag	ccccatgatt	acaacttctg	tctgtacccc	acagtacata											1033
accttagcc																1042

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<220>
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 <222> (43) .. (555)

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						Met	Arg	Leu	Pro							
						1										
gct	cag	ctc	ctg	ggg	ctg	cta	atg	ctc	tgg	gtc	cct	gga	tcc	agt	gag	102
Ala	Gln	Leu	Leu	Gly	Leu	Leu	Met	Leu	Trp	Val	Pro	Gly	Ser	Ser	Glu	
5					10					15					20	
gat	att	gtg	atg	acc	cag	act	cca	ctc	tcc	ctg	ccc	gtc	acc	cct	gga	150
Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Thr	Pro	Gly	
				25					30					35		
gag	ccg	gcc	tcc	atc	tcc	tgc	agg	tct	agt	cag	agc	ctc	ttg	gat	agt	198
Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	Asp	Ser	
			40					45					50			
gat	gat	gga	aac	acc	tat	ttg	gac	tgg	tac	ctg	cag	aag	cca	ggg	cag	246
Asp	Asp	Gly	Asn	Thr	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	
		55					60					65				
tct	cca	cag	ctc	ctg	atc	tat	acg	ctt	tcc	tat	cgg	gcc	tct	gga	gtc	294
Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Thr	Leu	Ser	Tyr	Arg	Ala	Ser	Gly	Val	
		70				75					80					
cca	gac	agg	ttc	agt	ggc	agt	ggg	tca	ggc	act	gat	ttc	aca	ctg	aaa	342
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	
		85				90				95					100	
atc	agc	agg	gtg	gag	gct	gag	gat	gtt	gga	gtt	tat	tac	tgc	atg	caa	390

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln	
105 110 115	
cgt ata gag ttt cct tgg act ttt ggc cag ggg acc aag ctg gag atc	438
Arg Ile Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile	
120 125 130	
aaa cga act gtt gct gca cca tct gtc ttc atc ttc ccg cca tct gat	486
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
135 140 145	
gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac	534
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn	
150 155 160	
ttc tat ccc aga gag gcc taa gt acagtggaaa gtggtaaacg gcctccaaac	587
Phe Tyr Pro Arg Glu Ala *	
165 170	
tggttaaadc cagtaaagtgc tcacagagca agacagtaag gacagcacct acgtactcag	647
cagcaaccag aagctgagca aagttgactt atgagatacc acaagtctag gcctgacgaa	707
gtcaaccatt atggacttgg gctgtgtcca atctgaatat agttatacct gggcagagtgc	767
gttaaaagggt atagtgtgtc ccctaaattg tatectaggt ttcaagctcg tagtcacttg	827
cccaggcttt ttgtcccttg taggtccttt tttcccaatg ggggacctaa gacactaagt	887
gacgggactc tccaaagtta atgatttaaa acttaaaatc actctctaag ggatcatcag	947
gagttatgaa gtcgatgact aattgttttt gatacagagta tatctgaaaa tgattgaaag	1007
tgtgaattcc tcatggtagg tgagataaac tagtcgttat agtatctagt agatgaccgg	1067
agcatttata gagtagaagt ccgcatactc ccggataatc taccacgaca catgattaga	1127
ctctcgcat ggtaaacaga tggatgtaaa ctcaatcgtg ggagtaccga aagagggtggc	1187
tatgatgttg acatgatagg gtctaggatg cgtgatcgtg tgacggaatt gtcaaatacg	1247
tgtgaataca catttattgg caatttctgt atgacgtgat atgagattag cagaggttta	1307
tgaatgagtg acatcttgcg tgtggt	1333

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 <211> 803
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (77)..(433)

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 Met Gly Pro Gly Leu Leu His Trp Met Ala Leu
 1 5 10
 tgt ctc ctt gga aca ggt cat ggg gat gcc atg gtc atc cag aac cca 157
 Cys Leu Leu Gly Thr Gly His Gly Asp Ala Met Val Ile Gln Asn Pro
 15 20 25
 aga tac cag gtt acc cag ttt gga aag cca gtg acc ctg agt tgt tct 205
 Arg Tyr Gln Val Thr Gln Phe Gly Lys Pro Val Thr Leu Ser Cys Ser
 30 35 40
 cag act ttg aac cat aac gtc atg tac tgg tac cag cag aag tca agt 253
 Gln Thr Leu Asn His Asn Val Met Tyr Trp Tyr Gln Gln Lys Ser Ser
 45 50 55
 cag gcc cca aag ctg ctg ttc cac tac tat gac aaa gat ttt aac aat 301
 Gln Ala Pro Lys Leu Leu Phe His Tyr Tyr Asp Lys Asp Phe Asn Asn
 60 65 70 75
 gaa gca gac acc cct gat aac ttc caa tcc agg agg ccg aac act tct 349
 Glu Ala Asp Thr Pro Asp Asn Phe Gln Ser Arg Arg Pro Asn Thr Ser
 80 85 90
 ttc tgc ttt ctt gac atc cgc tca cca ggc ctg ggg gac gca gcc atg 397
 Phe Cys Phe Leu Asp Ile Arg Ser Pro Gly Leu Gly Asp Ala Ala Met
 95 100 105
 tac ctg tgt gcc acc agc gtc cac cgg gac cca tga acac tgaagctttc 447
 Tyr Leu Cys Ala Thr Ser Val His Arg Asp Pro *
 110 115
 tttggacaag gcaccagact cacagttgta gcatgtgaaa aggtccagag ctctgcagtg 507
 tgagcttttct actgaaatgg cccttggact ttgtggttca ttcataactca gtggtctagc 567
 ttgtactact tttgagaatg caaagcttaa ctgtggacgg attccaatcc tggccaggca 627
 ggggttgctgg acactctgag agaagaaagg gttaatccca tgaccatcaa cttccatggg 687
 atttcagcca tcctggacaa gctaccacac cctcctgccc caaggggagg aggaaatgtg 747
 gaccatccca tcagaaattg accaaaggac ctgaacaagt ggtccccccc ccccc 803

<210> 312
 <211> 687
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (6)..(605)

<400> 312

agctg	atg ctc tgc aga caa caa ctc agg aat ttg act gaa aac aag	47
	Met Leu Cys Arg Gln Gln Leu Arg Asn Leu Thr Glu Asn Lys	
	1 5 10	
gaa tct gag ttg cag tgt ctc ttt caa cag ata gaa agg cag gag cag	95	
Glu Ser Glu Leu Gln Cys Leu Phe Gln Gln Ile Glu Arg Gln Glu Gln		
15 20 25 30		
ctt ctg gat gaa ata cat cgt gag aag aga gat cta ctg gaa gag acc	143	
Leu Leu Asp Glu Ile His Arg Glu Lys Arg Asp Leu Leu Glu Glu Thr		
35 40 45		
caa aga aaa gat gaa gaa atg gga tct ctg cag gac cgt gta att gca	191	
Gln Arg Lys Asp Glu Glu Met Gly Ser Leu Gln Asp Arg Val Ile Ala		
50 55 60		
tta gaa acg agt acc caa gtg gcc ttg gac cat ctg gag tct gtg cct	239	
Leu Glu Thr Ser Thr Gln Val Ala Leu Asp His Leu Glu Ser Val Pro		
65 70 75		
gag aaa ctg agc cta cta gaa gat ttc aaa gac ttc aga gat tcc tgc	287	
Glu Lys Leu Ser Leu Leu Glu Asp Phe Lys Asp Phe Arg Asp Ser Cys		
80 85 90		
agt tca tct gag aga act gat gga aga tat tcc aaa tac agg gtt cgc	335	
Ser Ser Ser Glu Arg Thr Asp Gly Arg Tyr Ser Lys Tyr Arg Val Arg		
95 100 105 110		
aga aat tct ctt cag cat cac caa gat gac acc aag tac aga acc aaa	383	
Arg Asn Ser Leu Gln His His Gln Asp Asp Thr Lys Tyr Arg Thr Lys		
115 120 125		
agt ttc aaa ggt gac aga acc ttt ctg gaa ggt tcc cac act cgt ggg	431	
Ser Phe Lys Gly Asp Arg Thr Phe Leu Glu Gly Ser His Thr Arg Gly		
130 135 140		
tta gat cac tca tcc tct tgg cag gat cac agt cgc ttc ctg tct agt	479	
Leu Asp His Ser Ser Ser Trp Gln Asp His Ser Arg Phe Leu Ser Ser		
145 150 155		
cca aga ttt tca tac gtg aac tca ttt acc aaa aga act gtt gct cca	527	
Pro Arg Phe Ser Tyr Val Asn Ser Phe Thr Lys Arg Thr Val Ala Pro		
160 165 170		
gat tca gct tca aac aag gaa gat gcc aca atg aat gga aca agt tca	575	
Asp Ser Ala Ser Asn Lys Glu Asp Ala Thr Met Asn Gly Thr Ser Ser		
175 180 185 190		
caa ccc aaa gag gaa tat ggg agc taa a aaagcaaag taatttggtta	626	
Gln Pro Lys Lys Glu Glu Tyr Gly Ser *		
195 200		
ttttacatga gtatgttaca aataataaca tctctattct tacagcaaaa aaaaaaaaaa	686	

<210> 313
 <211> 1157
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (714)..(947)

<400> 313

atttggccct cgaggccaag aattcggcac gaggatgaat aacaggataa cacgttggtta 60
 cattgtcaca actcctgatc caggaattga tggctaagat attcgtaatt cttatccttt 120
 tcagttgtaa cttattccta tttgtcagca ttcaggttat tagcggctgc tggcgaagtc 180
 cttgagaaat aaactgcaca ctggatggtg ggggtagtgt aggaaaatgg aggggaagga 240
 agtaaagttt caaattaagc ctgaacagca aagttcccct gagaaggcca cctggattct 300
 atcagaaact cgaatgtcca tcttgcaaaa cttccttgcc caaaccacac ccctggagtc 360
 acaaccacc cttgaccaat agattcattt cactgaggga ggcaaagggc tggtaaatag 420
 attcatttca ctgggagagg caaagggtct ggggccagag aggagaagta aaaagccaca 480
 catgaagcag caatgcaggc atgcttcttg ctcactctgtg atcaccagga aactcccaga 540
 tctgacactg tagtgcattt cactgctgac aagaaggctg ctgccaccag cctgtgaagc 600
 aaggttaagg tgagaaggct ggaggtgaga ttctgggcag tctcctgggt gtctacccat 660
 ggacctagag gtactttgaa agttttggat atctgggctc tgactgtgca ata atg 716
 Met
 1

ggc aac ccc aaa gtc aag gca cat ggc aag aag gtg ctg atc tcc ttc 764
 Gly Asn Pro Lys Val Lys Ala His Gly Lys Lys Val Leu Ile Ser Phe
 5 10 15

gga aaa gct gtt atg ctc acg gat gac ctc aaa ggc acc ttt gct aca 812
 Gly Lys Ala Val Met Leu Thr Asp Asp Leu Lys Gly Thr Phe Ala Thr
 20 25 30

ctg agt gac ctg cac tgt aac aag ctg cac gtg gac cct gag aac ttc 860
 Leu Ser Asp Leu His Cys Asn Lys Leu His Val Asp Pro Glu Asn Phe
 35 40 45

ctg ctc tta ggc aac gtg ata ttg att gtt ttg gca acc cac ttc agc 908
 Leu Leu Leu Gly Asn Val Ile Leu Ile Val Leu Ala Thr His Phe Ser
 50 55 60 65

gag gat ttt acc cta cag ata cag gct tct tgg cag taa ctaacaaatg 957
 Glu Asp Phe Thr Leu Gln Ile Gln Ala Ser Trp Gln *
 70 75

ctgtgggttaa tgctgtagcc cacaagacca ctgagttccc tgtccactat gtttgtacct 1017
 atgggccact atgtttgtac ctatgtccca aaatctcatc tccttttagat gggggagggtt 1077
 ggggagaaga gcagtatcct gcctgctgat tcagttcctg catgataaaa atagaataaaa 1137
 gaaatatgct ctctaagaaa 1157

<210> 314
 <211> 583
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (219)..(479)

<400> 314
 ctatgatctc tgaatccttg gatgccaccc caacacacct aacccccaac tctcaggcca 60
 agatagtaaa aagagagtca gagaacagga accgcataaa aagttcttca ttttccatca 120
 cttgggtggtg actttgaagg tagaggctga cagtgaagtgg agtatggaca tgtcacccac 180
 aaccagatga agaggggactc cgagatagcgc actcggct atg cac aca gtc acc 233
 Met His Thr Val Thr
 1 5

cac aga gga gga gca ggg aag ggg gaa agt agc ctc tct cag cac atg 281
 His Arg Gly Gly Ala Gly Lys Gly Glu Ser Ser Leu Ser Gln His Met
 10 15 20

ata aaa aga cct gga tgg gga ggt gga gca gag gcc ttc act cca tca 329
 Ile Lys Arg Pro Gly Trp Gly Gly Gly Ala Glu Ala Phe Thr Pro Ser
 25 30 35

ttt ttt aaa tcc atc ctt caa tat ttt caa gag gaa ggg aaa cca gac 377
 Phe Phe Lys Ser Ile Leu Gln Tyr Phe Gln Glu Glu Gly Lys Pro Asp
 40 45 50

agg cca aac cac agc ctt cag tgg ggc ttg act tta gtt cta cgg acc 425
 Arg Pro Asn His Ser Leu Gln Trp Gly Leu Thr Leu Val Leu Arg Thr
 55 60 65

tca cca gcc att cca gca gct gaa tgc ctg cca gtt ggt gcc cac acg 473
 Ser Pro Ala Ile Pro Ala Ala Glu Cys Leu Pro Val Gly Ala His Thr
 70 75 80 85

cta tga gacccccaaa ctgtgtgaga agctgggaac atttcacagg gaaaaagcag 529
 Leu *

aaatggaggg agtgaaaccc ctacttagtt tctgctgac ctcctggta gaga

583

<210> 315
<211> 931
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(677)

<400> 315

ggaattcggtt ttaagaggat cttctgctcc tcttcatctg gtccgtttcc ttccaaggcc 60

cccgagagga aggc atg cgg tgg gcc cta ctg gtg ctt cta gct ttc ctg 110

Met Arg Trp Ala Leu Leu Val Leu Leu Ala Phe Leu
1 5 10

tct cct gcc agt cag aaa tct tcc aac ttg gaa ggg aga acg aag tca 158

Ser Pro Ala Ser Gln Lys Ser Ser Asn Leu Glu Gly Arg Thr Lys Ser
15 20 25

gtc acc agg cag act ggg tca tct gct gaa atc act tgc gat ctt act 206

Val Thr Arg Gln Thr Gly Ser Ser Ala Glu Ile Thr Cys Asp Leu Thr
30 35 40

gta aca aat acc ttc tac atc cac tgg tac cta cac cag gag ggg aag 254

Val Thr Asn Thr Phe Tyr Ile His Trp Tyr Leu His Gln Glu Gly Lys
45 50 55 60

gcc cca cag cgt ctt ctg tac tat gac gtc tcc act gca agg gat gtg 302

Ala Pro Gln Arg Leu Leu Tyr Tyr Asp Val Ser Thr Ala Arg Asp Val
65 70 75

ttg gaa tca gga ctc agt cca gga aag tat tat act cat aca ccc agg 350

Leu Glu Ser Gly Leu Ser Pro Gly Lys Tyr Tyr Thr His Thr Pro Arg
80 85 90

agg tgg agc tgg ata ttg ata cta cga aat cta att gaa aat gat tct 398

Arg Trp Ser Trp Ile Leu Ile Leu Arg Asn Leu Ile Glu Asn Asp Ser
95 100 105

ggg gtc tat tac tgt gcc acc tgg gac agg cac agt gat tca gac ctg 446

Gly Val Tyr Tyr Cys Ala Thr Trp Asp Arg His Ser Asp Ser Asp Leu
110 115 120

tcc tac acc aca ctg aaa atc tgc ctt gtg gct gcc tct ggt tca cag 494

Ser Tyr Thr Thr Leu Lys Ile Cys Leu Val Ala Ala Ser Gly Ser Gln
125 130 135 140

gat aga gcc gcc ccc tct cat ttc ctg tca cca aat tta ctg tat tct 542

Asp Arg Ala Ala Pro Ser His Phe Leu Ser Pro Asn Leu Leu Tyr Ser

145	150	155	
gaa caa gag aaa gac agc tta act cct gat ctc cct cct aat atc aca			590
Glu Gln Glu Lys Asp Ser Leu Thr Pro Asp Leu Pro Pro Asn Ile Thr			
160	165	170	
ctg tcc tgg cag cag ctg cat cct gtt ccc cac ccc tcc ccc aca act			638
Leu Ser Trp Gln Gln Leu His Pro Val Pro His Pro Ser Pro Thr Thr			
175	180	185	
ttc ctg aag atc aag ctg cca tct cca ggc ctc agc taa gcagcctggc			687
Phe Leu Lys Ile Lys Leu Pro Ser Pro Gly Leu Ser *			
190	195	200	
tgagagcaag gttctctcag ctctcctagg acatggggga ggcccactca ctctgcttcc			747
tatgacacac aggtacaact aggggtccagc tgtgaagcga gatatttttg acagcaaag			807
ggaagggtat ttatactgaa tcatgtatcc actcatgggc cagagatcac agctgagagt			867
ggtgcttatt ccttatgtct ataacaacat aagcaatact ataatgacca ctaaaacact			927
aggc			931
<210>	316		
<211>	943		
<212>	DNA		
<213>	Homo sapiens		
<220>			
<221>	CDS		
<222>	(228) .. (737)		
<400>	316		
aatgccctcc acaagccaag cctcccgtc ttaggagctg agcatctgtc agctgcccaa			60
gcccggtggc tcttgatggg gtgtttgagc aaccatcctg tttttcgccc caggcccttg			120
gaattgaaag tgaggatgac ttgtataaac tgggtgaactt cttccttaaa tatcgagctc			180
accgtttatc ttccagcctc cagatcaagc cctgcagtca ggcgagc atg gag aag			236
		Met Glu Lys	
		1	
gcg agc atg gag gag aca agc acg agg tca gaa ttg gag ctg gca gag			284
Ala Ser Met Glu Glu Thr Ser Thr Arg Ser Glu Leu Glu Leu Ala Glu			
5	10	15	
cag acg gag atg gag gga gaa aag gaa gaa agc ctg gtg gaa ggg gag			332
Gln Thr Glu Met Glu Gly Glu Lys Glu Glu Ser Leu Val Glu Gly Glu			
20	25	30	35
aag gag gaa gag gag gag acc cca ccc tcc ccc tgg gtc atc cac ccc			380
Lys Glu Glu Glu Glu Glu Thr Pro Pro Ser Pro Trp Val Ile His Pro			

40	45	50	
aat gat gtc ctc aag att ctg gag gcc ttc ttc atg ggt ctg aag aag			428
Asn Asp Val Leu Lys Ile Leu Glu Ala Phe Phe Met Gly Leu Lys Lys			
55	60	65	
cct agg gac tcg cgg gcc ccg ctg agg gta cag aag aat gtg cgt gac			476
Pro Arg Asp Ser Arg Ala Pro Leu Arg Val Gln Lys Asn Val Arg Asp			
70	75	80	
aac tcc aag gac tcg gag tac tgg cag gcc ctg acc aca gtg atc cct			524
Asn Ser Lys Asp Ser Glu Tyr Trp Gln Ala Leu Thr Thr Val Ile Pro			
85	90	95	
tcc tcc aag cag aac ctc tgg gat gcc ctc tac aca gcc ttg gag aag			572
Ser Ser Lys Gln Asn Leu Trp Asp Ala Leu Tyr Thr Ala Leu Glu Lys			
100	105	110	115
tac cac ctt gtc ctg acc cag agg gcc aag ctg ctg ctg gaa aac agt			620
Tyr His Leu Val Leu Thr Gln Arg Ala Lys Leu Leu Leu Glu Asn Ser			
120	125	130	
tct ctg gag cag cag aac aca gag ctg cag gcg cta ctg cag cag tat			668
Ser Leu Glu Gln Gln Asn Thr Glu Leu Gln Ala Leu Leu Gln Gln Tyr			
135	140	145	
ctg aac tcc aag atc aac tct gaa ctg caa gtt cct ccc act cag gtg			716
Leu Asn Ser Lys Ile Asn Ser Glu Leu Gln Val Pro Pro Thr Gln Val			
150	155	160	
ttg cgg gta ccc aca aaa tga gc tggaccgcca aaggetgatg tgtagggct			769
Leu Arg Val Pro Thr Lys *			
165	170		
ggcctgatgc tgggtgtctgt gccggagcca gctcatatca cccactgggc cgcacctggg			829
cctgctctct ggattttcca gggctgtctt tatagcctgt cgaaataagg agccagagga			889
gttacctgtg tcctgcatta tgattaaagc cttttaaggt tgaaaaaaaa aaaa			943

<210> 317
 <211> 793
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (339)..(623)

<400> 317	
ttaatacgac cactataggg aatttggccc tcgagcgacg taattcggca cgagagaacg	60
gactactggg cttttaaaaa cacacctcac caagctcagc caccaactta aaaaggactt	120

gataatactt ttaccacttg cccttctcag aattcgggcc tgtcttcgga atgcgacagg 180
 atacagccca tttgagctcc tgtatagatg ctccttttta ttaggccccca gtctcattcc 240
 agacaccaga ccaacttggga ctgtgcccccc aaaaacttgt catccctact atcttctctc 300
 tagtcatact cctattcacc gttctcaact actcatac atg ccc tgc tct tgt 353
 Met Pro Cys Ser Cys
 1 5
 tta cac tgc cgg ttt aca ctg ttt ctc caa gcc atc aca gct gat atc 401
 Leu His Cys Arg Phe Thr Leu Phe Leu Gln Ala Ile Thr Ala Asp Ile
 10 15 20
 tcc tgg tgc tat cct caa act acc act ctt aac tcc ctc ttg gat ttg 449
 Ser Trp Cys Tyr Pro Gln Thr Thr Thr Leu Asn Ser Leu Leu Asp Leu
 25 30 35
 tta tat gat ctt tgc cgg cag gca ccc ctc caa tac ttt cac cct gat 497
 Leu Tyr Asp Leu Cys Arg Gln Ala Pro Leu Gln Tyr Phe His Pro Asp
 40 45 50
 gaa gtt cta ttc ttt act ttt ata ctc act ctt att ctc att ccc att 545
 Glu Val Leu Phe Phe Thr Phe Ile Leu Thr Leu Ile Leu Ile Pro Ile
 55 60 65
 ctt atg cca ccc ttt acc tct ccc cag cta tct cca cca cac tat caa 593
 Leu Met Pro Pro Phe Thr Ser Pro Gln Leu Ser Pro Pro His Tyr Gln
 70 75 80 85
 tct cac tgt ctc tct cct agc cat ttc taa t ccttctttaa caaacaattg 644
 Ser His Cys Leu Ser Pro Ser His Phe *
 90 95
 ctggccttgc atttctcttt cctctaaaac cactgaggcc tcaacttact cactgctgaa 704
 aaaggaggac ttttcatatt tctaaatgaa gaatgttggt tttacctaaa tcaatctggc 764
 ctagtacctg acaacataaa aaaaaaaaaa 793

<210> 318
 <211> 1024
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (28) ..(366)

<400> 318
 gtggggcggc ggctgcagc cagcaag atg tac cac tgc agc gag tgc ctg 51
 Met Tyr His Cys Ser Glu Cys Leu
 1 5

cgc ttc ttc cag cag cgc aag agc ctg ctg ctg cac cag cgc ctg cac 99
 Arg Phe Phe Gln Gln Arg Lys Ser Leu Leu Leu His Gln Arg Leu His
 10 15 20

acc ggc aat ggc cag ggc tgg ccc gcc tgc ccc tac tgc ggc aag gcc 147
 Thr Gly Asn Gly Gln Gly Trp Pro Ala Cys Pro Tyr Cys Gly Lys Ala
 25 30 35 40

ttc cgc cgg ccc tcg gac ctc ttc cgg cac cag cgc atc cac acc ggt 195
 Phe Arg Arg Pro Ser Asp Leu Phe Arg His Gln Arg Ile His Thr Gly
 45 50 55

gag cgg ccc tac cag tgc ccc cag tgt ggc cgg acc ttc aac cgc aac 243
 Glu Arg Pro Tyr Gln Cys Pro Gln Cys Gly Arg Thr Phe Asn Arg Asn
 60 65 70

cac cac ctg gcc gtg cac atg cag acc cac gcc cga ggc cag gtg ggc 291
 His His Leu Ala Val His Met Gln Thr His Ala Arg Gly Gln Val Gly
 75 80 85

cca cac ttc cct gcc gcc ccc gcc cgc cac ggg agc ctg ccc ctg ccc 339
 Pro His Phe Pro Ala Ala Pro Ala Arg His Gly Ser Leu Pro Leu Pro
 90 95 100

tgg ccc agc cgg aag gag gag ggc tga cctgg caggagccca cagaggaccc 391
 Trp Pro Ser Arg Lys Glu Gly *
 105 110

ctggcggggt ctctcccctg tgcctgacgc aggttcttcc ttttcctggg atggagagag 451

gtttgttggt tttacccatt caaatgggaa gctagctgcc cttctggtga cattgtgtgt 511

gaccgggtgc tttctgtttc ctgtttgcac tcttcgctgc cttttctgca ttcctgactt 571

ctaaaagatg ccttaaggct taagggatgc catatttttg ataaggcctc tggtaggtac 631

cacagccaag aggaccagag atcatggccc ttccagtatg ggggcgatag agacatcggg 691

gacctgggat ctcagttttg tgcagagatc tcctgcctgc tgtcaccatg agaaacagtg 751

gagtggagtg gatggatggc ctgacttgaa gaaagggccc tggaaagttt tctactttgc 811

tatattgaaa tataaatccc ttcttataga gactttgaaa tacttctgta aatgtgtgta 871

gtagtcaatg gaactttgcc tttagcaaag tcggaaagag tcggcttttc catgtgaggc 931

tcgcagagct gaaaggggag ctacgtccac caagcctgta ggtcataagg gacacaaaca 991

aggacgagga agaggaccct taaagaacgg acc 1024

<210> 319
 <211> 2552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (281)..(2518)

<400> 319

tttaaaggca aagacacgcc ttcccccccc acttcagccg cgcgcctttc cttcccccaa	60
attcctcaaa gatggtttgt ctcacgtggt gcagggcgta aaagcggctt gcattcaatt	120
agcagcgaag ctcgcgggcg ctggcgggac aggcgcgtga ggccacaaca catgcgtgta	180
tcttgcttgg gctatcttcc ctgctctgcc acgccgggtc tggagaaggg gtttcagccc	240
caggacattt actgagagtc ggcgaaatatt gggagccgcg atg ttc ccc ctt cgg	295
Met Phe Pro Leu Arg	
1 5	
gcc ctg tgg ttg gtc tgg gcg ctt cta gga gtg gcc gga tca tgc ccg	343
Ala Leu Trp Leu Val Trp Ala Leu Leu Gly Val Ala Gly Ser Cys Pro	
10 15 20	
gag ccg tgc gcc tgc gtg gac aag tac gct cac cag ttc gcg gac tgc	391
Glu Pro Cys Ala Cys Val Asp Lys Tyr Ala His Gln Phe Ala Asp Cys	
25 30 35	
gct tac aaa gag ttg cgt gag gtg ccg gaa gga ctg cct gcc aac gtg	439
Ala Tyr Lys Glu Leu Arg Glu Val Pro Glu Gly Leu Pro Ala Asn Val	
40 45 50	
acg acg ctt agt ctg tcc gcg aac aag atc act gtg ctg cgg cgc ggg	487
Thr Thr Leu Ser Leu Ser Ala Asn Lys Ile Thr Val Leu Arg Arg Gly	
55 60 65	
gcc ttc gcc gac gtc aca cag gtc acg tcg ctg tgg ctg gcg cac aat	535
Ala Phe Ala Asp Val Thr Gln Val Thr Ser Leu Trp Leu Ala His Asn	
70 75 80 85	
gag gtg cgc acc gtg gag cca ggc gca ctg gcc gtg ctg agt cag ctc	583
Glu Val Arg Thr Val Glu Pro Gly Ala Leu Ala Val Leu Ser Gln Leu	
90 95 100	
aag aac ctc gat ctg agc cac aac ttc ata tcc agc ttt ccg tgg agc	631
Lys Asn Leu Asp Leu Ser His Asn Phe Ile Ser Ser Phe Pro Trp Ser	
105 110 115	
gac ctg cgc aac ctg agc gcg ctg cag ctg ctc aaa atg aac cac aac	679
Asp Leu Arg Asn Leu Ser Ala Leu Gln Leu Leu Lys Met Asn His Asn	
120 125 130	
cgc ctg ggc tct ctg ccc cgg gac gca ctc ggt gcg cta ccc gac ctg	727
Arg Leu Gly Ser Leu Pro Arg Asp Ala Leu Gly Ala Leu Pro Asp Leu	
135 140 145	
cgt tcc ctg cgc atc aac aac aac cgg ctg cgt acg ctg gcg cct ggc	775
Arg Ser Leu Arg Ile Asn Asn Asn Arg Leu Arg Thr Leu Ala Pro Gly	
150 155 160 165	

acc ttc gac gcg ctt agc gcg ctg tca cac ttg caa ctc tat cac aat	823
Thr Phe Asp Ala Leu Ser Ala Leu Ser His Leu Gln Leu Tyr His Asn	
170 175 180	
ccc ttc cac tgc ggc tgc ggc ctt gtg tgg ctg cag gcc tgg gcc gcg	871
Pro Phe His Cys Gly Cys Gly Leu Val Trp Leu Gln Ala Trp Ala Ala	
185 190 195	
agc acc cgg gtg tcc tta ccc gag ccc gac tcc att gct tgt gcc tcg	919
Ser Thr Arg Val Ser Leu Pro Glu Pro Asp Ser Ile Ala Cys Ala Ser	
200 205 210	
cct ccc gcg ctg cag ggg gtg ccg gtg tac cgc ctg ccc gcc ctg ccc	967
Pro Pro Ala Leu Gln Gly Val Pro Val Tyr Arg Leu Pro Ala Leu Pro	
215 220 225	
tgt gca ccg ccc agc gtg cat ctg agt gcc gag cca ccg ctt gaa gca	1015
Cys Ala Pro Pro Ser Val His Leu Ser Ala Glu Pro Pro Leu Glu Ala	
230 235 240 245	
ccc ggc acc cca ctg cgc gca gga ctg gcg ttc gtg tta cac tgc atc	1063
Pro Gly Thr Pro Leu Arg Ala Gly Leu Ala Phe Val Leu His Cys Ile	
250 255 260	
gcc gac ggc cac cct acg cct cgc ctg caa tgg caa ctt cag atc ccc	1111
Ala Asp Gly His Pro Thr Pro Arg Leu Gln Trp Gln Leu Gln Ile Pro	
265 270 275	
ggc ggc acc gta gtc tta gag cca ccg gtt ctg agc ggg gag gac gac	1159
Gly Gly Thr Val Val Leu Glu Pro Pro Val Leu Ser Gly Glu Asp Asp	
280 285 290	
ggg gtt ggg gcg gag gaa gga gag gga gaa gga gat ggg gat ttg ctg	1207
Gly Val Gly Ala Glu Glu Gly Glu Gly Glu Gly Asp Gly Asp Leu Leu	
295 300 305	
acg cag acc caa gcc caa acg ccg act cca gca ccc gct tgg ccg gcg	1255
Thr Gln Thr Gln Ala Gln Thr Pro Thr Pro Ala Pro Ala Trp Pro Ala	
310 315 320 325	
ccc cca gcc aca ccg cgc ttc ctg gcc ctc gca aat ggc tcc ctg ttg	1303
Pro Pro Ala Thr Pro Arg Phe Leu Ala Leu Ala Asn Gly Ser Leu Leu	
330 335 340	
gtg ccc ctc ctg agt gcc aag gag gcg ggc gtc tac act tgc cgt gca	1351
Val Pro Leu Leu Ser Ala Lys Glu Ala Gly Val Tyr Thr Cys Arg Ala	
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cac aat gag ctg ggc gcc aac tct acg tca ata cgc gtg gcg gtg gca	1399
His Asn Glu Leu Gly Ala Asn Ser Thr Ser Ile Arg Val Ala Val Ala	
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gca acc ggg ccc cca aaa cac gcg cct ggc gcc ggg gga gaa ccc gac	1447
Ala Thr Gly Pro Pro Lys His Ala Pro Gly Ala Gly Gly Glu Pro Asp	
375 380 385	

Cys	His	Leu	Leu	Ala	Lys	His	Pro	Gly	Lys	Pro	Tyr	Arg	Leu	Ile	Leu		
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cg	g	c	c	c	g	c	a	g	a	c	a	g	c	a	g	t	2215
Arg	Pro	Gln	Ala	Pro	Asp	Pro	Met	Glu	Lys	Arg	Ile	Ala	Ala	Asp	Phe		
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Asp	Pro	Arg	Ala	Ser	Tyr	Leu	Glu	Ser	Glu	Lys	Ser	Tyr	Pro	Ala	Gly		
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ggc	gag	gcg	ggc	ggc	gag	gag	cca	gag	gac	gtg	cag	ggg	gag	ggc	ctt		2311
Gly	Glu	Ala	Gly	Gly	Glu	Glu	Pro	Glu	Asp	Val	Gln	Gly	Glu	Gly	Leu		
			665						670						675		
gat	gaa	gac	gcg	ggg	cag	gga	gac	cca	agt	ggg	gac	ctg	cag	aga	gag		2359
Asp	Glu	Asp	Ala	Gly	Gln	Gly	Asp	Pro	Ser	Gly	Asp	Leu	Gln	Arg	Glu		
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gag	agc	ctg	gcg	gcc	tgc	tca	ctg	gtg	gag	tcc	cag	tcc	aag	gcc	aac		2407
Glu	Ser	Leu	Ala	Ala	Cys	Ser	Leu	Val	Glu	Ser	Gln	Ser	Lys	Ala	Asn		
		695					700										
caa	gag	gag	ttc	gag	gcg	ggc	tct	gag	tac	agc	gat	cgg	ctg	ccc	ctg		2455
Gln	Glu	Glu	Phe	Glu	Ala	Gly	Ser	Glu	Tyr	Ser	Asp	Arg	Leu	Pro	Leu		
710						715				720					725		
ggc	gcc	gag	gcg	gtc	aac	atc	gcc	cag	gag	att	aat	ggc	aac	tac	agg		2503
Gly	Ala	Glu	Ala	Val	Asn	Ile	Ala	Gln	Glu	Ile	Asn	Gly	Asn	Tyr	Arg		
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Gln	Thr	Ala	Gly	*													
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cggcggcctt	ccccgggtc	tgtctgccaa	a	atg	tct	gaa	aga	tca	gat	ctc							232
				Met	Ser	Glu	Arg	Ser	Asp	Leu							

1										5						
ctt	cac	ttc	aag	ttt	gaa	aat	tat	gga	gat	tca	atg	tta	caa	aaa	atg	280
Leu	His	Phe	Lys	Phe	Glu	Asn	Tyr	Gly	Asp	Ser	Met	Leu	Gln	Lys	Met	
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aac	aaa	tta	aga	gaa	gag	aat	aaa	ttt	tgt	gat	gtt	aca	gtt	ctc	ata	328
Asn	Lys	Leu	Arg	Glu	Glu	Asn	Lys	Phe	Cys	Asp	Val	Thr	Val	Leu	Ile	
25							30			35						
gat	gat	att	gag	gta	cag	gga	cat	aaa	att	gtg	ttt	gct	gca	ggg	tcc	376
Asp	Asp	Ile	Glu	Val	Gln	Gly	His	Lys	Ile	Val	Phe	Ala	Ala	Gly	Ser	
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ccc	ttc	tta	aga	gac	caa	ttt	tta	ctg	aat	gat	tcc	aga	gag	gtg	aaa	424
Pro	Phe	Leu	Arg	Asp	Gln	Phe	Leu	Leu	Asn	Asp	Ser	Arg	Glu	Val	Lys	
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atc	tcc	ata	tta	cag	agt	tcc	gaa	gtg	ggg	aga	caa	ttg	ctc	tta	tcc	472
Ile	Ser	Ile	Leu	Gln	Ser	Ser	Glu	Val	Gly	Arg	Gln	Leu	Leu	Leu	Ser	
75			80				85									
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Cys	Tyr	Ser	Gly	Val	Leu	Glu	Phe	Pro	Glu	Met	Glu	Leu	Val	Asn	Tyr	
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Leu	Thr	Ala	Ala	Ser	Phe	Leu	Gln	Met	Ser	His	Ile	Val	Glu	Arg	Cys	
105			110				115									
aca	cag	gcc	ctg	tgg	aag	ttt	ata	aag	cca	aaa	caa	cca	atg	gat	agt	616
Thr	Gln	Ala	Leu	Trp	Lys	Phe	Ile	Lys	Pro	Lys	Gln	Pro	Met	Asp	Ser	
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Lys	Glu	Gly	Cys	Glu	Pro	Gln	Ser	Ala	Ser	Pro	Gln	Ser	Lys	Glu	Gln	
140			145				150									
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Gln	Gly	Asp	Ala	Arg	Gly	Ser	Pro	Lys	Gln	Asp	Ser	Pro	Cys	Ile	His	
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cca	tct	gaa	gac	agt	atg	gat	atg	gag	gac	agt	gat	att	cag	att	gtt	760
Pro	Ser	Glu	Asp	Ser	Met	Asp	Met	Glu	Asp	Ser	Asp	Ile	Gln	Ile	Val	
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aag	gta	gaa	tct	att	ggg	gat	gta	tca	gag	gtt	aga	agt	aaa	aaa	gat	808
Lys	Val	Glu	Ser	Ile	Gly	Asp	Val	Ser	Glu	Val	Arg	Ser	Lys	Lys	Asp	
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Gln	Asn	Gln	Phe	Ile	Ser	Ser	Glu	Pro	Thr	Ala	Leu	His	Ser	Ser	Glu	
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Pro	Gln	His	Ser	Leu	Ile	Asn	Ser	Thr	Val	Glu	Asn	Arg	Val	Ser	Glu	

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235																240	245	
gat Asp	aac Asn	atc Ile	atc Ile	atg Met	gcc Ala	tca Ser	aaa Lys	gat Asp	gtc Val	ttt Phe	ggc Gly	cct Pro	aat Asn	att Ile	cga Arg	1000		
250																255	260	
ggt Gly	gta Val	gac Asp	aaa Lys	ggc Gly	cta Leu	cag Gln	tgg Trp	cat His	cac His	cag Gln	tgc Cys	cca Pro	aag Lys	tgt Cys	acc Thr	1048		
265																270	275	
agg Arg	gtg Val	ttt Phe	cgt Arg	cac His	ctg Leu	gag Glu	aac Asn	tac Tyr	gcc Ala	aac Asn	cat His	tta Leu	aaa Lys	atg Met	cac His	1096		
280																285	290	295
aaa Lys	ctc Leu	ttt Phe	atg Met	tgt Cys	cta Leu	ctc Leu	tgc Cys	ggc Gly	aag Lys	act Thr	ttc Phe	act Thr	cag Gln	aaa Lys	ggc Gly	1144		
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aac Asn	ctt Leu	cat His	cga Arg	cac His	atg Met	cgt Arg	gtg Val	cat His	gcc Ala	gga Gly	att Ile	aaa Lys	cct Pro	ttc Phe	cag Gln	1192		
315																320	325	
tgt Cys	aaa Lys	atc Ile	tgt Cys	ggg Gly	aaa Lys	acc Thr	ttt Phe	tct Ser	cag Gln	aag Lys	tgt Cys	tcc Ser	tta Leu	cag Gln	gat Asp	1240		
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cat His	ctt Leu	aac Asn	ctt Leu	cac His	agt Ser	gga Gly	gat Asp	aag Lys	ccc Pro	cat His	aaa Lys	tgt Cys	aac Asn	tat Tyr	tgt Cys	1288		
345																350	355	
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360																365	370	375
ctg Leu	cat His	ggc Gly	aaa Lys	aac Asn	agc Ser	ttt Phe	gat Asp	aat Asn	gcc Ala	aat Asn	gag Glu	aga Arg	aat Asn	gta Val	caa Gln	1384		
380																385	390	
gac Asp	ctc Leu	aca Thr	gtg Val	gat Asp	ttt Phe	gat Asp	tct Ser	ttt Phe	gca Ala	tgt Cys	aca Thr	aca Thr	gtc Val	aca Thr	gac Asp	1432		
395																400	405	
tct Ser	aaa Lys	ggg Gly	tgt Cys	cag Gln	cca Pro	caa Gln	ccc Pro	gat Asp	gca Ala	aca Thr	cag Gln	gtc Val	ctg Leu	gat Asp	gca Ala	1480		
410																415	420	
ggt Gly	aaa Lys	ctg Leu	gcc Ala	caa Gln	gct Ala	gtc Val	ctg Leu	aac Asn	tta Leu	aga Arg	aat Asn	gat Asp	agt Ser	act Thr	tgt Cys	1528		
425																430	435	
gtg Val	aat Asn	tga *	gtagggg	cttc	atgccc	acaactc	gaa	ctgactg	gaca	atgtgg	gcaat					1584		
440																		

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<213> Homo sapiens

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tcttcccagg gagctgaaaa gccagattcg acctggtagc caagca atg tca cag 175
                                     Met Ser Gln
                                     1
cag aag cag caa tct tgg aag cct cca aat gtt ccc aaa tgc tcc cct 223
Gln Lys Gln Gln Ser Trp Lys Pro Pro Asn Val Pro Lys Cys Ser Pro
      5              10              15
ccc caa aga tca aac ccc tgc cta gct ccc tac tcg act cct tgt ggt 271
Pro Gln Arg Ser Asn Pro Cys Leu Ala Pro Tyr Ser Thr Pro Cys Gly
      20              25              30              35

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gct ccc cat tca gaa ggt tgt cat tcc agt tcc caa agg cct gag gtt	319
Ala Pro His Ser Glu Gly Cys His Ser Ser Ser Gln Arg Pro Glu Val	
40 45 50	
cag aag cct agg agg gct cgt caa aag ctg cgc tgc cta agt agg ggc	367
Gln Lys Pro Arg Arg Ala Arg Gln Lys Leu Arg Cys Leu Ser Arg Gly	
55 60 65	
aca acc tac cac tgc aaa gag gaa gag tgt gaa ggc gac tga gccaga	416
Thr Thr Tyr His Cys Lys Glu Glu Glu Cys Glu Gly Asp *	
70 75 80	
agagttgagg cacaggtgca gttactctct ccctgcccc cctttgggta ctaattcccc	476
cttgaaagc caggccctca acctctcatt tggactgaga aacacttcct gatccccagc	536
tctagagaag cgagaactag gctgagccac gctgctactg ctctcttcca ttcacccctt	596
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tcacctaacc catttggtgc ttcctctacc tgtgtcagc c atg gcc agc gag	173
Met Ala Ser Glu	
1	
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Ser Ser Pro Leu Leu Ala Tyr Arg Leu Leu Gly Glu Glu Gly Val Ala	
5 10 15 20	
ctc cct gcc aat ggg gcc ggg ggt cct gga ggg gcg tct gcc cgg aag	269
Leu Pro Ala Asn Gly Ala Gly Gly Pro Gly Gly Ala Ser Ala Arg Lys	
25 30 35	
ctg tcc acc ttc ctg ggt gtg gtg gtg ccc act gtc ctg tcc atg ttc	317
Leu Ser Thr Phe Leu Gly Val Val Val Pro Thr Val Leu Ser Met Phe	
40 45 50	
agc ata gtt gtt ttt ctg agg att ggg ttc gtg gtg ggt cat gct ggg	365
Ser Ile Val Val Phe Leu Arg Ile Gly Phe Val Val Gly His Ala Gly	
55 60 65	

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ctc acc gtc ctc tct gtc tgt gcc atc gcc acc aat gga gcc gtg cag Leu Thr Val Leu Ser Val Cys Ala Ile Ala Thr Asn Gly Ala Val Gln 85 90 95 100	461
ggg ggc gga gcc tac ttc atg atc agc cgc aca ctg ggg ccc gag gtc Gly Gly Gly Ala Tyr Phe Met Ile Ser Arg Thr Leu Gly Pro Glu Val 105 110 115	509
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gcc gtc tcc ctc ctg ggg ctg gtg gag tct gtg ctt gat gtc ttc ggg Ala Val Ser Leu Leu Gly Leu Val Glu Ser Val Leu Asp Val Phe Gly 135 140 145	605
gcc gat gcc aca ggg ccc agt ggg ctc cgg gtc ctg ccc cag ggc tac Ala Asp Ala Thr Gly Pro Ser Gly Leu Arg Val Leu Pro Gln Gly Tyr 150 155 160	653
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gct gtg ggg ccg agg gac atc cgc ttg act cct agg cct ggc ccc aat Ala Val Gly Pro Arg Asp Ile Arg Leu Thr Pro Arg Pro Gly Pro Asn 215 220 225	845
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Asp Pro Ser Arg Ala Ile Pro Leu Gly Thr Ile Val Ala Val Ala Tyr
 295 300 305

acc ttc ttc gtc tat gtc ctg ctt ttc ttt ctc tcc agc ttc act tgt 1133
 Thr Phe Phe Val Tyr Val Leu Leu Phe Phe Leu Ser Ser Phe Thr Cys
 310 315 320

gac agg acc ctg ctg cag gaa gac tat ggg ttc ttc cgc gcc atc agc 1181
 Asp Arg Thr Leu Leu Gln Glu Asp Tyr Gly Phe Phe Arg Ala Ile Ser
 325 330 335 340

ctg tgg ccc cca ctg gtg ttg atc gga atc tat gcc aca gcg ctc tca 1229
 Leu Trp Pro Pro Leu Val Leu Ile Gly Ile Tyr Ala Thr Ala Leu Ser
 345 350 355

gcg tcc atg agc tcg ctc att ggt gcc tcc cgc atc ctc cat gcc ctg 1277
 Ala Ser Met Ser Ser Leu Ile Gly Ala Ser Arg Ile Leu His Ala Leu
 360 365 370

gcc cgg gat gac ctc ttt ggc gtg atc ttg gca ccg gcc aag gtt gtg 1325
 Ala Arg Asp Asp Leu Phe Gly Val Ile Leu Ala Pro Ala Lys Val Val
 375 380 385

tcc cga ggg gga aac ccc tgg gca gct gta ctt tat tct tgg ggc ctg 1373
 Ser Arg Gly Gly Asn Pro Trp Ala Ala Val Leu Tyr Ser Trp Gly Leu
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gtg cag ctg gtg ctc ctg gct ggg aag ctg aac aca ctg gcc gct gtg 1421
 Val Gln Leu Val Leu Leu Ala Gly Lys Leu Asn Thr Leu Ala Ala Val
 405 410 415 420

gtc act gtc ttc tac ctg gtg gcc tat gct gcc gtg gac ctg tcc tgc 1469
 Val Thr Val Phe Tyr Leu Val Ala Tyr Ala Ala Val Asp Leu Ser Cys
 425 430 435

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 Leu Ser Leu Glu Trp Ala Ser Ala Pro Asn Phe Arg Pro Thr Phe Ser
 440 445 450

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 Leu Phe Ser Trp His Thr Cys Leu Leu Gly Val Ala Ser Cys Leu Leu
 455 460 465

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 Met Met Phe Leu Ile Ser Pro Gly Ala Ala Gly Gly Ser Leu Leu Leu
 470 475 480

atg ggt ctg ctg gct gcc ctg ctc acc gcg cga gga ggc ccc agt agc 1661
 Met Gly Leu Leu Ala Ala Leu Leu Thr Ala Arg Gly Gly Pro Ser Ser
 485 490 495 500

tgg ggc tat gtc agc cag gcc ttg ctt ttc cac cag gtg cgt aag tat 1709
 Trp Gly Tyr Val Ser Gln Ala Leu Leu Phe His Gln Val Arg Lys Tyr
 505 510 515

ctg ctt cgg ctg gac gtc cgg aag gat cac gtg aag ttc tgg cgg ccc 1757
 Leu Leu Arg Leu Asp Val Arg Lys Asp His Val Lys Phe Trp Arg Pro

520	525	530	
cag ctg ctg ctc ctg gtg ggg aac	ccc cgg ggc gcc	ctg cct ctg ctg	1805
Gln Leu Leu Leu Leu Val Gly	Asn Pro Arg Gly Ala	Leu Pro Leu Leu	
535	540	545	
cgg ttg gcc aac cag ctt aag aag	ggg ggg ctg tat	gtg ctg ggc cac	1853
Arg Leu Ala Asn Gln Leu Lys	Lys Gly Gly Leu Tyr	Val Leu Gly His	
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gtc acc ctg gga gac ctc gac tcc	ctg ccc tgc gac cct	gta cag ccg	1901
Val Thr Leu Gly Asp Leu Asp	Ser Leu Pro Ser Asp	Pro Val Gln Pro	
565	570	575	580
cag tat ggg gca tgg ctc agc ctg	gtg gac cgt gcc	cag gtg aag gct	1949
Gln Tyr Gly Ala Trp Leu Ser	Leu Val Asp Arg Ala	Gln Val Lys Ala	
585	590	595	
ttt gtg gat cta acc ttc tca ccc	tcc gtg cgc cag ggg	gct cag cat	1997
Phe Val Asp Leu Thr Phe Ser	Pro Ser Val Arg Gln	Gly Ala Gln His	
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Leu Leu Arg Ile Ser Gly Leu	Gly Gly Met Lys Pro	Asn Thr Leu Val	
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Leu Gly Phe Tyr Asp Asp Ala	Pro Pro Gln Asp His	Phe Leu Thr Asp	
630	635	640	
ccg gct ttc tct gag cct gca gac	agc acc agg gag ggc	agt tcc cca	2141
Pro Ala Phe Ser Glu Pro Ala	Asp Ser Thr Arg Glu	Gly Ser Ser Pro	
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gct ctg agc acc ctg ttc cct cct	ccc cgg gct cct ggg	agc ccc cgg	2189
Ala Leu Ser Thr Leu Phe Pro	Pro Pro Pro Arg Ala	Pro Gly Ser Pro	
665	670	675	
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Ala Leu Asn Pro Gln Asp Tyr	Val Ala Thr Val Ala	Asp Ala Leu Lys	
680	685	690	
atg aac aag aat gtg gtg ctg gcc	cgg gcc agc ggg gcc	ttg ccc cct	2285
Met Asn Lys Asn Val Val Leu	Ala Arg Ala Ser Gly	Ala Leu Pro Pro	
695	700	705	
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Glu Arg Leu Ser Arg Gly Ser	Gly Gly Thr Ser Gln	Leu His His Val	
710	715	720	
gac gtg tgg ccc ctc aac ttg ttg	cgg ccc cgg ggt ggg	ccc ggc tat	2381
Asp Val Trp Pro Leu Asn Leu	Leu Arg Pro Arg Gly	Gly Pro Gly Tyr	
725	730	735	740
gtg gat gtc tgc ggc ctc ttc ctg	ctg cag atg gca acc	atc ttg ggc	2429
Val Asp Val Cys Gly Leu Phe	Leu Leu Gln Met Ala	Thr Ile Leu Gly	
745	750	755	

atg gtg ccc gct tgg cat agc gcc cgg ctc cgg atc ttc ctg tgc ctg 2477
Met Val Pro Ala Trp His Ser Ala Arg Leu Arg Ile Phe Leu Cys Leu
760 765 770

ggg cct cgg gag gcg cct ggg gcg gcc gag ggg cgg ctg cgg gca ctg 2525
Gly Pro Arg Glu Ala Pro Gly Ala Ala Glu Gly Arg Leu Arg Ala Leu
775 780 785

ctg agc caa ctg agg atc cgg gct gag gtg cag gag gtg gtg tgg ggc 2573
Leu Ser Gln Leu Arg Ile Arg Ala Glu Val Gln Glu Val Val Trp Gly
790 795 800

gag ggg gcc ggg gct ggg gaa ccc gag gcg gag gag gaa ggg gac ttt 2621
Glu Gly Ala Gly Ala Gly Glu Pro Glu Ala Glu Glu Glu Gly Asp Phe
805 810 815 820

gtg aac agt ggg cgg gga gac gca gag gca gag gcc ctg gca cgc agc 2669
Val Asn Ser Gly Arg Gly Asp Ala Glu Ala Glu Ala Leu Ala Arg Ser
825 830 835

gcc aac gcc ctg gtt cgg gcc cag cag ggg cgc ggc aca gga gga ggg 2717
Ala Asn Ala Leu Val Arg Ala Gln Gln Gly Arg Gly Thr Gly Gly Gly
840 845 850

ccg ggt ggg ccg gag ggt ggg gat gct gag ggc ccc atc aca gcc ctc 2765
Pro Gly Gly Pro Glu Gly Gly Asp Ala Glu Gly Pro Ile Thr Ala Leu
855 860 865

acc ttc ctg tac ttg cct cgg ccg cca gcc gat ccc gcc cga tac ccc 2813
Thr Phe Leu Tyr Leu Pro Arg Pro Pro Ala Asp Pro Ala Arg Tyr Pro
870 875 880

cgc tac ctg gcg cta ctg gag act cta acc cga gac ctg ggc ccc acg 2861
Arg Tyr Leu Ala Leu Leu Glu Thr Leu Thr Arg Asp Leu Gly Pro Thr
885 890 895 900

ctg ctg gtt cat ggg gtc act cca gtc acc tgc act gat ctg tga 2906
Leu Leu Val His Gly Val Thr Pro Val Thr Cys Thr Asp Leu *
905 910 915

<210> 323
<211> 607
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (78)..(416)

<400> 323
actagcgtgg ttccagtgtc gtcacgcgtg ctaaaaaagg gggtttcccg tgacaggccc 60

cgacagagga gcaggcc	atg agg cag gca gga gcc acg tat ctg ggc cca	110
	Met Arg Gln Ala Gly Ala Thr Tyr Leu Gly Pro	
	1 5 10	
gcg cac ccg cca agc tct cta gcc tct cct ggc ctc agt ata ctt ctc	158	
Ala His Pro Pro Ser Ser Leu Ala Ser Pro Gly Leu Ser Ile Leu Leu		
	15 20 25	
tgg gag atg gtc cag ctg aaa atc ccc agc atc cac aag aaa ggg tgg	206	
Trp Glu Met Val Gln Leu Lys Ile Pro Ser Ile His Lys Lys Gly Trp		
	30 35 40	
aag ccc tgg ggg ccc tgg cct ggc cca ggt gca ggc tgc atg gcc ggg	254	
Lys Pro Trp Gly Pro Trp Pro Gly Pro Gly Ala Gly Cys Met Ala Gly		
	45 50 55	
cgg agc ggt gtc tcc ttt cac agc ttc ccc gtc tgt ccg cag cct cca	302	
Arg Ser Gly Val Ser Phe His Ser Phe Pro Val Cys Pro Gln Pro Pro		
	60 65 70 75	
gga gcc cca cac agg gct ggg gct ctg tgc ccc caa ctc aca ccc gtc	350	
Gly Ala Pro His Arg Ala Gly Ala Leu Cys Pro Gln Leu Thr Pro Val		
	80 85 90	
ggc tcc ccc agg agg agc agg ctg ggc cca gag ccg cag ggt ggg ctg	398	
Gly Ser Pro Arg Arg Ser Arg Leu Gly Pro Glu Pro Gln Gly Gly Leu		
	95 100 105	
cag gga ggt ctg act tag ctgggg aaagtgccat ccctgccatt gctagtgaca	452	
Gln Gly Gly Leu Thr *		
	110	
agctcgggct gctgtggccc cagcacagat tcaacactca ctgcgctacg tgccagctgt	512	
tgcacactca cctccacacc caactcacag gaagcaaggc tgggaaggag ggaactggcc	572	
ccaggccaca cagatgctgc gagttgggat tatga	607	

<210> 324
 <211> 505
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)..(252)

<400> 324	
ccctgattag tgtataaatt tgaatatctt tcatatttat tggctattgg gatttcctct	60
gccataactt ga	
atg tta gga tct act ggt tat ttt tat ttc ctt gcc	108
Met Leu Gly Ser Thr Gly Tyr Phe Tyr Phe Leu Ala	
1 5 10	

gat ttg ctg ata tta aca ata gat ttt aat ctc ttg tta ata ata tac	156
Asp Leu Leu Ile Leu Thr Ile Asp Phe Asn Leu Leu Leu Ile Ile Tyr	
15 20 25	
ctt gca aac tac ttt tct cag tct gtg gct tat ctt ttc att tct tta	204
Leu Ala Asn Tyr Phe Ser Gln Ser Val Ala Tyr Leu Phe Ile Ser Leu	
30 35 40	
tgg gtt ttc ttt ggc atg agg gta caa gtt tta ctt tta atg aag taa	252
Trp Val Phe Phe Gly Met Arg Val Gln Val Leu Leu Met Lys *	
45 50 55 60	
aatatgtaac ttacattac agtttgtgct tatttgtatt acttatgaaa catttccta	312
cccagaagtc atgaaggat tctcctctat ttccttctag aagtttggct cttcagattt	372
ccaatgttcc tgaaattaac ttctatgtag ggtgaggtag caaccaatt ttattttctt	432
ccatataatc acttgaccta gcaaaatata attgcctatt ctttcccaa tgatctacaa	492
tgccatattt agt	505

<210> 325
 <211> 670
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (232) .. (624)

<400> 325	
ccggatactg cccgggtcga cccacgcgtc cggtagacag ggagctgtga cgagagcaag	60
aggtcataac acatccagac tccttaagag aaagcctttc tgttttggaa acttttcaaa	120
gccagggact tgtccagccc aacctcccca ttgctcctag ctctgaggc tcaggacccc	180
tggcttctgt cctccctgct cagggtcctg cagcgttgcc tctgctcagc c atg ctc	237
Met Leu	
1	
ctg ctg ctc gtc cca gtg ctc gag gtg att ttt act ctg gga gga acc	285
Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly Gly Thr	
5 10 15	
aga gcc cag tcg gtg acc cag ctt gac agc cac gtc tct gtc tct gaa	333
Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val Ser Glu	
20 25 30	
gga acc ccg gtg ctg ctg agg tgc aac tac tca tct tct tat tca cca	381
Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr Ser Pro	
35 40 45 50	

tct ctc ttc tgg tat gtg caa cac ccc aac aaa gga ctc cag ctt ctc	429
Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln Leu Leu	
55 60 65	
ctg aag tac aca tca gcg gcc acc ctg gtt aaa ggc atc aac ggt ttt	477
Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn Gly Phe	
70 75 80	
gag gct gaa ttt aag aag agt gaa acc tcc ttc cac ctg acg aaa ccc	525
Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr Lys Pro	
85 90 95	
tca gcc cat atg agc gac gcg gct gag tac ttc tgt gtt gtg agt gac	573
Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val Ser Asp	
100 105 110	
aca gtg ctt gag act gca gga gag ctg aac aca agc ctc ctg aga tgc	621
Thr Val Leu Glu Thr Ala Gly Glu Leu Asn Thr Ser Leu Leu Arg Cys	
115 120 125 130	
tga gactttctgt gactcaagaa ctcgaccttg aagtctgttt tataat	670
*	

<210> 326
 <211> 794
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (200)..(304)

<220>
 <221> misc_feature
 <222> (1)...(794)
 <223> n = a,t,c or g

<400> 326	
gtcagcaatg gtctcatgga agagggaagc tttattttaca ccatcaaggg cccatggatg	60
accacagtc tgtgtgactg ctgtgtgatt ggttttcaga cattagcttt aataggaatc	120
ataggagaag ggacatggtg gctactgcaa ggggtttttt tgtttaggga gaacgcactg	180
tggaactcaa attccgggt atg cac tca acc tcg gca aag gca cct cgc tgt	232
Met His Ser Thr Ser Ala Lys Ala Pro Arg Cys	
1 5 10	
tgg tca cac ccc gtg agt ttt tgt ggt tta cta att gtc ctc tct gga	280
Trp Ser His Pro Val Ser Phe Cys Gly Leu Leu Ile Val Leu Ser Gly	
15 20 25	

```

aag aaa tcc aat ggg acc tgt tga aacacagctg aatttaattg ctatgcttag 334
Lys Lys Ser Asn Gly Thr Cys *
      30              35

catgcagttg ttaactatgt ctgatgtgtg agcaagatat gaatacatgt ttccctggag 394

gctggatttg gttatcaggt ctcggggcag tttgataaat tgtactaatg ctgcaatcac 454

tgtttttcaa aggtccacaa agcacgttgt ggcttttgga aaggcagaga taagaagcaa 514

agctttgtga tagagacaga aacaaggcca tgaaaaggga agctaccaaaa gcaatggcat 574

agccaaggaa gtgtgtcttc acaagataag tggcaaggac cctgttgagt tgatgcttgt 634

gttgtttggt agaattaaaa attaagatga gtgggttggc cccagtgggc catgcctgta 694

attccctcac tttgggaggc tgaggcaggt ggatagctga ggtcaagagt tcaagaccac 754

gaaatcgtcg acagcgannc nttccgggaa ttccggacgg 794

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<210> 327
<211> 507
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (44)..(472)

```

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<400> 327
tttcgtgaaa attttaatcc tcagtgaacc agggcagaaa aga  atg atg ata tcc 55
                                     Met Met Ile Ser
                                     1

ttg aga gtt tta ctg gtg atc ctg tgg ctt cag tta agc tgg gtt tgg 103
Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu Ser Trp Val Trp
  5              10              15              20

agc caa cgg aag gag gtg gag cag gat cct gga ccc ttc aat gtt cca 151
Ser Gln Arg Lys Glu Val Glu Gln Asp Pro Gly Pro Phe Asn Val Pro
      25              30              35

gag gga gcc act gtc gct ttc aac tgt act tac agc aac agt gct tct 199
Glu Gly Ala Thr Val Ala Phe Asn Cys Thr Tyr Ser Asn Ser Ala Ser
      40              45              50

cag tct ttc ttc tgg tac aga cag gat tgc agg aaa gaa cct aag ttg 247
Gln Ser Phe Phe Trp Tyr Arg Gln Asp Cys Arg Lys Glu Pro Lys Leu
      55              60              65

ctg atg tcc gta tac tcc agt ggt aat gaa gat gga agg ttt aca gca 295
Leu Met Ser Val Tyr Ser Ser Gly Asn Glu Asp Gly Arg Phe Thr Ala
      70              75              80

```

cag ctc aat aga gcc agc cag tat att tcc ctg ctc atc aga gac tcc	343
Gln Leu Asn Arg Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp Ser	
85 90 95 100	
aag ctc agt gat tca gcc acc tac ctc tgt gtg gtg aac att cgc cca	391
Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Val Val Asn Ile Arg Pro	
105 110 115	
gga aac aca cct ttg gga ctg gaa caa gac ttc agg tca cgc tcg ata	439
Gly Asn Thr Pro Leu Gly Leu Glu Gln Asp Phe Arg Ser Arg Ser Ile	
120 125 130	
tcc aga acc ctg acc ctg ccg tgt acc agc tga gagactct aaatccagt	490
Ser Arg Thr Leu Thr Leu Pro Cys Thr Ser *	
135 140	
acaatgctgt cgaccta	507

<210> 328
 <211> 1043
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (210)..(1043)

<400> 328	
accggtccgg aattcccggg tcgacgattt cgtccggtgt cggaagcac cagtgccctg	60
aggaagggcc atttccaaaa gccctgtgct gacacagggt tgctggttcc tcttcaagag	120
cccactctct ggggtggggc catatctcca gcagaggtgg gctggaaagg acccccccaa	180
tcccgccgc cgtgagctta gctggagcc atg gcc tct gca ccc atc tcg atg	233
Met Ala Ser Ala Pro Ile Ser Met	
1 5	
ctt gcg atg ctc ttc aca ttg agt ggg ctg aga gct cag tca gtg gct	281
Leu Ala Met Leu Phe Thr Leu Ser Gly Leu Arg Ala Gln Ser Val Ala	
10 15 20	
cag ccg gaa gat cag gtc aac gtt gct gaa ggg aat cct ctg act gtg	329
Gln Pro Glu Asp Gln Val Asn Val Ala Glu Gly Asn Pro Leu Thr Val	
25 30 35 40	
aaa tgc acc tat tca gtc tct gga aac cct tat ctt ttt tgg tat gtt	377
Lys Cys Thr Tyr Ser Val Ser Gly Asn Pro Tyr Leu Phe Trp Tyr Val	
45 50 55	
caa tac ccc aac cga ggc ctc cag ttc ctt ctg aaa tac atc aca ggg	425
Gln Tyr Pro Asn Arg Gly Leu Gln Phe Leu Leu Lys Tyr Ile Thr Gly	
60 65 70	

<211> 1037
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(831)

<400> 329

atg agc atc agc ctc ctg tgc tgt gca gcc ttt cct ctc ctg tgg gca	48
Met Ser Ile Ser Leu Leu Cys Cys Ala Ala Phe Pro Leu Leu Trp Ala	
1 5 10 15	
ggt cca gtg aat gct ggt ggt gtc act cag acc cca aaa ttc cgc atc	96
Gly Pro Val Asn Ala Gly Gly Val Thr Gln Thr Pro Lys Phe Arg Ile	
20 25 30	
ctg aag ata gga cag agc atg aca ctg cag tgt gcc cag gat atg aac	144
Leu Lys Ile Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn	
35 40 45	
cat aac tac atg tac tgg tat cga caa gac cca ggc atg ggg ctg aag	192
His Asn Tyr Met Tyr Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Lys	
50 55 60	
ctg att tat tat tca gtt ggt gct ggt atc act gac aaa gga gaa gtc	240
Leu Ile Tyr Tyr Ser Val Gly Ala Gly Ile Thr Asp Lys Gly Glu Val	
65 70 75 80	
ccg aat ggc tac aac gtc tcc aga tca acc aca gag gat ttc ccg ctc	288
Pro Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu	
85 90 95	
agg ctg gag ttg gct gct ccc tcc cag aca tct gtg tac ttc tgt gcc	336
Arg Leu Glu Leu Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala	
100 105 110	
agc agt agg ggt ggg gcc ggg ctc aat gag cag ttc ttc ggg cca ggg	384
Ser Ser Arg Gly Gly Ala Gly Leu Asn Glu Gln Phe Phe Gly Pro Gly	
115 120 125	
aca cgg ctc acc gtg cta gag gac ctg aaa aac gtg ttc cca ccc gag	432
Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu	
130 135 140	
gtc gct gtg ttt gag cca tca gaa gca gag atc tcc cac acc caa aag	480
Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys	
145 150 155 160	
gcc aca ctg gta tgc ctg gcc aca ggc ttc tac ccc gac cac gtg gag	528
Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu	
165 170 175	
ctg agc tgg tgg gtg aat ggg aag gag gtg cac agt ggg gtc agc aca	576
Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr	
180 185 190	

gac ccg cag ccc ctc aag gag cag ccc gcc ctc aat gac tcc aga tac	624
Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr	
195 200 205	
tgc ctg agc agc cgc ctg agg gtc tcg gcc acc ttc tgg cag aac ccc	672
Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro	
210 215 220	
cgc aac cac ttc cgc tgt caa gtc cag ttc tac ggg ctc tcg gag aat	720
Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn	
225 230 235 240	
gac gag tgg acc cag gat agg gcc aaa cct gtc acc cag atc gtc agc	768
Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser	
245 250 255	
gcc gag gcc tgg ggt aga gca ggt gag tgg ggc ctg ggg aga tgc ctg	816
Ala Glu Ala Trp Gly Arg Ala Gly Glu Trp Gly Leu Gly Arg Cys Leu	
260 265 270	
gag gag att agg tga gaccagctac cagggaat ggaaagatcc aggtagcga	871
Glu Glu Ile Arg *	
275	
caagactata tccagaagaa agccagagtg gacaagggtgg gatgatcaag gttcacaggg	931
tcagcaaagc acggtgtgca cttccccac caagaagcat ataggctgaa tggagcacct	991
caagctcatt cttccttcag atcctgacac cttagagcta agcttt	1037
<210> 330	
<211> 738	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (300)..(608)	
<400> 330	
tagttcaaag aagaaaagtc agctggatgt gatgcctcat gcctgtaatc ctaccacttt	60
gggaggccaa cacggttga tctcttgagc ccaggagtgc gagactagcc tggccaacat	120
ggcgaaaccc cttctctttt tcttttttta aaatttttta gttagaaatg aaaaaaagaa	180
agaagtctag gttttctgaa acaagcactg tcttggtgct accttttttc atgtgtggac	240
acatagaaaag cgaggatatt tgtacagcac cttgaaacaa ataagcagga ggtgatgtc	299
atg agc ctt agc cct gca ggg acc aga cta ggc ctt ctg aag ctg agg	347
Met Ser Leu Ser Pro Ala Gly Thr Arg Leu Gly Leu Leu Lys Leu Arg	
1 5 10 15	
tgg tcc ttg tcc cca cac ctt gta acc cat ttc cag ccc atg ggt gtc	395

Trp	Ser	Leu	Ser	Pro	His	Leu	Val	Thr	His	Phe	Gln	Pro	Met	Gly	Val		
			20					25					30				
agt	tgg	gaa	att	cta	cac	aag	atc	cta	gta	gat	gta	att	aca	tat	aat		443
Ser	Trp	Glu	Ile	Leu	His	Lys	Ile	Leu	Val	Asp	Val	Ile	Thr	Tyr	Asn		
		35					40					45					
tca	atg	gtt	ttt	gat	gat	ggg	gtt	tta	aaa	tca	agt	tat	tca	ata	ggt		491
Ser	Met	Val	Phe	Asp	Asp	Gly	Val	Leu	Lys	Ser	Ser	Tyr	Ser	Ile	Gly		
		50				55					60						
ggg	gtg	cag	tgg	ctc	acg	cct	gta	att	cca	gca	ctt	tgg	gag	gcc	gag		539
Gly	Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Glu	Ala	Glu		
		65			70				75					80			
gag	ggc	aga	tca	caa	ggt	cgg	gag	ttc	aag	acc	agc	ctg	acc	aac	atg		587
Glu	Gly	Arg	Ser	Gln	Gly	Arg	Glu	Phe	Lys	Thr	Ser	Leu	Thr	Asn	Met		
				85				90						95			
gta	aaa	ctc	cgt	ctc	tac	taa	aa	attcaaaaaat	tagccggccg	tggtggtgga							640
Val	Lys	Leu	Arg	Leu	Tyr	*											
				100													
catctgtaat	cccagctact	tagggggctg	aggcaggaga	atcgcttgaa	cgggggacagg												700
tcggggcagg	gcggaactc	cctcttaaaa	aaaaaaaaa														738

<210> 331
 <211> 679
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (243)..(449)

<220>
 <221> misc_feature
 <222> (1)...(679)
 <223> n = a,t,c or g

<400>	331																
aacaagcagc	agtgaggaca	ccaaagccaa	gccacgccac	ccgggcccgc	ccccaggaca												60
cggagtttaa	ggaccgcgtc	tcccagatg	ccagaggagac	ctgcgtccgc	actgccccag												120
tgtgacccgc	atacctaccg	gccccgaccc	cgaaccgcgt	ggcgtccgcc	cgagccctgg												180
cgctgctggg	tctcctgctg	ctgccgctgc	tcgcagagcc	caggaaactc	tgcccgcagc												240
tt	atg	acg	gtc	att	aac	cag	ttt	ctg	acc	aag	gac	aag	gac	acc	tac		287
	Met	Thr	Val	Ile	Asn	Gln	Phe	Leu	Thr	Lys	Asp	Lys	Asp	Thr	Tyr		
	1				5					10					15		

atg gac act gtc aac aga tac cac ctc acg gag ccg gaa aga aac aca 335
Met Asp Thr Val Asn Arg Tyr His Leu Thr Glu Pro Glu Arg Asn Thr
20 25 30

tcc tct aaa ctc aag gac tgc gtg acc gac aca atg acc ccc gag gag 383
Ser Ser Lys Leu Lys Asp Cys Val Thr Asp Thr Met Thr Pro Glu Glu
35 40 45

aca gag gcc gtc gtg cag caa ctg gaa gaa atc aac aac cag tgt gcc 431
Thr Glu Ala Val Val Gln Gln Leu Glu Glu Ile Asn Asn Gln Cys Ala
50 55 60

gac acg ata ctg aag taa caccat ccataggcac ctcgggttcc tgtccaggct 485
Asp Thr Ile Leu Lys *
65

gcctgtccca accatgagaa tctgggcca gggccccacc ctccctagct cccgccctgc 545

tgctgcctct actctctctc ctgctgtgct gattggggca agcctgggaa cggctgcccc 605

ccacctcccc acccaggncc tgtcctgcgg gacaatgctg cctaataaac tcacctgcat 665

ccaaaaaaaaa aaaa 679

<210> 332
<211> 445
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (200)..(400)

<400> 332

cttttagtcca gcgtggtgga attcgtagat ccccgctggtg caccagccct tctgccacag 60

ctgccattgg agagcagcag ccatggctct gtgctacca ctatggccgt gtgccttgac 120

aagggccaca agatgaccaa gaacatgagc aagcccaggc acagctgccg ccgcggggcg 180

ctgaccaaac accaaattc atg tgg gac atg atc cga gag gtg tgt ggt ttc 232
Met Trp Asp Met Ile Arg Glu Val Cys Gly Phe
1 5 10

gcc ccg tat gag cgg cac gcc atg gtg tta ctc aag gtc tcc aag gac 280
Ala Pro Tyr Glu Arg His Ala Met Val Leu Leu Lys Val Ser Lys Asp
15 20 25

aaa cgg gcc ctc aag ttc atc aag aaa aga gtg ggg aca cac atc cgc 328
Lys Arg Ala Leu Lys Phe Ile Lys Lys Arg Val Gly Thr His Ile Arg
30 35 40

act aag agg agg cag gag gag ctg agc aat gtc cca gcc atc atg agg 376
Thr Lys Arg Arg Gln Glu Glu Leu Ser Asn Val Pro Ala Ile Met Arg

45	50	55	
aaa gct gat gcc aag aaa gac tga gccccctgtc ctgccctctc tctgaaataa			430
Lys Ala Asp Ala Lys Lys Asp *			
60	65		

agaacacctt gacag	445
------------------	-----

<210> 333
 <211> 1716
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (633)..(1433)

<400> 333	
cccggttcga cgattcgtag gatattccaag ggacctcagg ctgtgggctg ggcttcaggg	60
aggagagccag agggtcagtg tccctagagg atccccaggg aagtgccaaag gaggagaagg	120
aatgtcctgg ctgacctaaag ggacgacaga agattgggga agagggggta tcaggaagaa	180
atgggttttca gttcagttta acaaacatct attgtgtgtt cactggggcca ggccagtgct	240
aggtgctagg gagacagagg tgaagagcct gccctctagc agctgacagc ctggcaaaaa	300
aataagacag aataaggtag accctgattt tggaacctga agaccaaagt gcaagattag	360
ctctgctact tccatctgtg gaccattggg caggtatctc tgggccttca cttactcttt	420
gtgaaatgag gacaggggca atccctaccc taccaagtca ttgggagtgag agacatgatg	480
acacggtgat tgtgaaaaga ttttgtcaat cgcaccagca ttaagggtgc ccatctccag	540
gttccccag gcctcaaggc tccaaggcc tgagtgggca ggtagcacc aggtatagac	600
cttcacgtg cagcaccag gacacagcca gc atg aac tgg gca ttt ctg cag	653
	Met Asn Trp Ala Phe Leu Gln
	1 5
ggc ctg ctg agt ggc gtg aac aag tac tcc aca gtg ctg agc cgc atc	701
Gly Leu Leu Ser Gly Val Asn Lys Tyr Ser Thr Val Leu Ser Arg Ile	
10 15 20	
tgg ctg tct gtg gtg ttc atc ttt cgt gtg ctg gtg tac gtg gtg gca	749
Trp Leu Ser Val Val Phe Ile Phe Arg Val Leu Val Tyr Val Val Ala	
25 30 35	
gcg gag gag gtg tgg gac gat gag cag aag gac ttt gtc tgc aac acc	797
Ala Glu Glu Val Trp Asp Asp Glu Gln Lys Asp Phe Val Cys Asn Thr	
40 45 50 55	

aag cag ccc ggc tgc ccc aac gtc tgc tat gac gag ttc ttc ccc gtg	845
Lys Gln Pro Gly Cys Pro Asn Val Cys Tyr Asp Glu Phe Phe Pro Val	
60 65 70	
tcc cac gtg cgc ctc tgg gcc cta cag ctc atc ctg gtc acg tgc ccc	893
Ser His Val Arg Leu Trp Ala Leu Gln Leu Ile Leu Val Thr Cys Pro	
75 80 85	
tca ctg ctc gtg gtc atg cac gtg gcc tac cgc gag gaa cgc gag cgc	941
Ser Leu Leu Val Val Met His Val Ala Tyr Arg Glu Glu Arg Glu Arg	
90 95 100	
aag cac cac ctg aaa cac ggg ccc aat gcc ccg tcc ctg tac gac aac	989
Lys His His Leu Lys His Gly Pro Asn Ala Pro Ser Leu Tyr Asp Asn	
105 110 115	
ctg agc aag aag cgg ggc gga ctg tgg tgg acg tac ttg ctg agc ctc	1037
Leu Ser Lys Lys Arg Gly Gly Leu Trp Trp Thr Tyr Leu Leu Ser Leu	
120 125 130 135	
atc ttc aag gcc gcc gtg gat gct ggc ttc ctc tat atc ttc cac cgc	1085
Ile Phe Lys Ala Ala Val Asp Ala Gly Phe Leu Tyr Ile Phe His Arg	
140 145 150	
ctc tac aag gat tat gac atg ccc cgc gtg gtg gcc tgc tcc gtg gag	1133
Leu Tyr Lys Asp Tyr Asp Met Pro Arg Val Val Ala Cys Ser Val Glu	
155 160 165	
cct tgc ccc cac act gtg gac tgt tac atc tcc ccg ccc acg gag aag	1181
Pro Cys Pro His Thr Val Asp Cys Tyr Ile Ser Arg Pro Thr Glu Lys	
170 175 180	
aag gtc ttc acc tac ttc atg gtg acc aca gct gcc atc tgc atc ctg	1229
Lys Val Phe Thr Tyr Phe Met Val Thr Thr Ala Ala Ile Cys Ile Leu	
185 190 195	
ctc aac ctc agt gaa gtc ttc tac ctg gtg ggc aag agg tgc atg gag	1277
Leu Asn Leu Ser Glu Val Phe Tyr Leu Val Gly Lys Arg Cys Met Glu	
200 205 210 215	
atc ttc ggc ccc agg cac cgg cgg cct cgg tgc cgg gaa tgc cta ccc	1325
Ile Phe Gly Pro Arg His Arg Arg Pro Arg Cys Arg Glu Cys Leu Pro	
220 225 230	
gat acg tgc cca cca tat gtc ctc tcc cag gga ggg cac cct gag gat	1373
Asp Thr Cys Pro Pro Tyr Val Leu Ser Gln Gly Gly His Pro Glu Asp	
235 240 245	
ggg aac tct gtc cta atg aag gct ggg tcg gcc cca gtg gat gca ggt	1421
Gly Asn Ser Val Leu Met Lys Ala Gly Ser Ala Pro Val Asp Ala Gly	
250 255 260	
ggg tat cca taa cct gcgagatcag cagataagat caacagggtcc cccccacatg	1476
Gly Tyr Pro *	
265	
aggccaccca ggaaaaaagg caggggacagt ggcacacctg ccgtagcagg gtgggtgagga	1536

gggtggctgt gggggctcag gaagctcgcc caggggcca tgtgggaggt tgggggtagt 1596
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 Met Tyr Cys Cys
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 Ala Leu Arg Ser Cys Ser Val Pro Thr Gly Pro Ala Thr Thr Phe Cys
 5 10 15 20
 tca ttt gat aaa agc tgc cgc tgt gga gtc tgc cta ccc agc acc tgc 151
 Ser Phe Asp Lys Ser Cys Arg Cys Gly Val Cys Leu Pro Ser Thr Cys
 25 30 35
 cca cat gag atc agc ctc ctt cag ccc atc tgc tgt gac acc tgc ccc 199
 Pro His Glu Ile Ser Leu Leu Gln Pro Ile Cys Cys Asp Thr Cys Pro
 40 45 50
 cca ccc tgc tgc aag cct gat acc tat gtg cca act tgc tgg ctg ctc 247
 Pro Pro Cys Cys Lys Pro Asp Thr Tyr Val Pro Thr Cys Trp Leu Leu
 55 60 65
 aac aac tgt cac ccg act ccc gga ctg agt ggg atc aac ctg acc acc 295
 Asn Asn Cys His Pro Thr Pro Gly Leu Ser Gly Ile Asn Leu Thr Thr
 70 75 80
 tat gtt cag cct ggc tgt gag agt ccc tgt gag ccc cgc tgt taa cca 343
 Tyr Val Gln Pro Gly Cys Glu Ser Pro Cys Glu Pro Arg Cys *
 85 90 95
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 cagc 407

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                  1                      5                      10

ttc acc gtg cac ctg ggg cgc cag aag acg gtg gtg ctg acg ggg ttc      100
Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr Gly Phe
                  15                      20                      25

gag gcg gtc aaa gag gcg ctg gcg ggc ccc ggg cag gag ctg gcc gac      148
Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu Ala Asp
                  30                      35                      40

cgg cct ccc atc gcc atc ttc cag ctc atc cag cga ggt gga ggc atc      196
Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly Gly Ile
                  45                      50                      55

ttc ttc tca tct ggg gcg cgc tgg agg gct gcc cgc cag ttc acg gtg      244
Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe Thr Val
                  60                      65                      70

cgt gcc ctg cac agc ctg ggc gtg ggc cgg gag ccg gtg gct gac aag      292
Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala Asp Lys
                  75                      80                      85                      90

att ctg cag gag ctg aaa tgc ctc tct ggg cag ctg gat ggc tac aga      340
Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly Tyr Arg
                  95                      100                      105

ggc cgg ccc ttc ccg ctg gcc cta ctg ggc tgg gct ccc tcc aat atc      388
Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser Asn Ile
                  110                      115                      120

acc ttc gcg ctc ctc ttc ggc cgc cga ttt gac tac cgg gac ccc gtg      436
Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp Pro Val
                  125                      130                      135

ttt gtg tcc ctg ctg ggt ctc atc gat gag gtc atg gtc ctc ttg ggg      484
Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu Leu Gly
                  140                      145                      150

tcc cct ggc ctg cag ctg ttc aac gtc cac cca tgg ctc ggg gcc ctg      532
Ser Pro Gly Leu Gln Leu Phe Asn Val His Pro Trp Leu Gly Ala Leu
                  155                      160                      165                      170

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ctc cag ctg cac cgg ccc gtc ctg cgc aag atc gag gag gtc cgt gcc	580
Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val Arg Ala	
175 180 185	
att ctg agg acc ctc ctg gag gcg cgg agg ccc cac gtg tgc ccg ggg	628
Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys Pro Gly	
190 195 200	
gac ccc gtg tgc agc tat gtg gac gcc ctg atc cag cag gga cag ggg	676
Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly Gln Gly	
205 210 215	
gat gac ccc gag ggc ctg ttt gct gag gcc aac gcg gtg gcc tgc acc	724
Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala Cys Thr	
220 225 230	
ctg gac atg gtc atg gcc ggg acg gag acg acc tcg gcc acg ctg cag	772
Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr Leu Gln	
235 240 245 250	
tgg gcc gca ctt ctg atg ggc cgg cac ccg gac gtg cag ggc cgg gtg	820
Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly Arg Val	
255 260 265	
cag gag gag cta gac cgc gtg ctg ggc cct ggg cgg act ccc cgg ctg	868
Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro Arg Leu	
270 275 280	
gag gac cag cag gct ctg ccc tac aca agc gcc gtg ctc cac gag gtg	916
Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His Glu Val	
285 290 295	
cag cgg ttc atc acg ctc ctg ccg cac gtg ccc cgc tgc acc gcg gcc	964
Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr Ala Ala	
300 305 310	
gac aca cag ctg ggc ggc ttc ctg ctc ccc aag ggc acg ccc gtg att	1012
Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro Val Ile	
315 320 325 330	
ccc ctg ctg acc tcg gtg ctc ctg gat gag aca cag tgg cag acc cca	1060
Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln Thr Pro	
335 340 345	
ggc cag ttc aac ccc ggc cat ttc ctg gac gcg aat ggg cac ttt gtg	1108
Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His Phe Val	
350 355 360	
aag cgg gag gcc ttc ctg cct ttc tct gca ggt cag cag ccc tcg ggg	1156
Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Gln Gln Pro Ser Gly	
365 370 375	
ccg ggg tgg ggc ggc acc tcc agg gct cca ggg gtg gga cgg ccc cag	1204
Pro Gly Trp Gly Gly Thr Ser Arg Ala Pro Gly Val Gly Arg Pro Gln	
380 385 390	
ctc cgc ctg ccg cct ctg cac cca cct cct gat ctc agg ttc tga agg	1252

Leu Arg Leu Pro Pro Leu His Pro Pro Pro Asp Leu Arg Phe *
 395 400 405

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 gactcctgca gacccactc cattcccgt cctggaacac ttctgcagc tgtgcctgga 2032
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<222> (107)..(322)

<400> 336

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caatgccaac atctgagcaa acattttggg gtatatctct attttc atg ttt aca 115
Met Phe Thr
1

ttg tcg ttt aaa aaa caa tca aac gac att agc agt ttt aca aca ttt 163
Leu Ser Phe Lys Lys Gln Ser Asn Asp Ile Ser Ser Phe Thr Thr Phe
5 10 15

tcc ttt cca gtt aaa act gta tac cgt tac cat ttt ccc atc ata ctc 211
Ser Phe Pro Val Lys Thr Val Tyr Arg Tyr His Phe Pro Ile Ile Leu
20 25 30 35

ttc acc tac gat act gtt tta agt ggc tgt ata gat ttc cac ttt cac 259
Phe Thr Tyr Asp Thr Val Leu Ser Gly Cys Ile Asp Phe His Phe His
40 45 50

aac aga att agc aga ttc cca aaa ctt gaa tat tta att tta aaa aaa 307
Asn Arg Ile Ser Arg Phe Pro Lys Leu Glu Tyr Leu Ile Leu Lys Lys
55 60 65

att ctt aat aac tga tattaaattt atatacgcaa atctgacaca ttacttcctt 362
Ile Leu Asn Asn *
70

aggataaatt cctgtacgca cagtctttcc attttaagcc tattatacta tgaaggagtc 422

tgaatcaaca tctaagagct ccgagagttc aacaccagcc tgggccatat tgtgagaaca 482

cgtctctaca gacgatcaaa aaattagctt ggtgtggtgg cgcgcgcctg tgatctcagc 542

taccaggag gctgaggtgg gaggatcact taagcccggg aggtcgagggc tgctgtgagc 602

cgtgagccac tgatcatacc actgcactcc agtctgggca acagagcgat cctgtttcag 662

agaaaaaaaa gatccaagac ctctgtagac cacactgaca gccctgctac tatttgcaac 722

tggtcgcgcc ctcgtgccga attcttggcc tcgagggcca aat 765

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<220>

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<222> (528)..(695)

<400> 337

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cca	gca	gct	ttt	cca	aag	gac	aat	atc	cat	ttc	aag	cct	ata	aat	aca		206
Pro	Ala	Ala	Phe	Pro	Lys	Asp	Asn	Ile	His	Phe	Lys	Pro	Ile	Asn	Thr		
				30					35					40			
aat	ctt	gat	agg	gca	aat	gaa	ttg	gca	aaa	aca	gac	att	ttg	agt	cta		254
Asn	Leu	Asp	Arg	Ala	Asn	Glu	Leu	Ala	Lys	Thr	Asp	Ile	Leu	Ser	Leu		
			45					50					55				
aca	agt	caa	aac	aag	acc	ttt	gat	ccc	aag	aaa	gaa	aat	ccc	att	gtg		302
Thr	Ser	Gln	Asn	Lys	Thr	Phe	Asp	Pro	Lys	Lys	Glu	Asn	Pro	Ile	Val		
		60					65					70					
tta	ctt	agt	gac	ttt	tac	tat	gga	cag	cat	aaa	gga	gaa	ggg	cag	ccg		350
Leu	Leu	Ser	Asp	Phe	Tyr	Tyr	Gly	Gln	His	Lys	Gly	Glu	Gly	Gln	Pro		
	75					80					85						
gaa	cag	aag	act	cac	acc	acc	ttt	aaa	tgc	ctc	agc	tgc	gtg	aaa	gtt		398
Glu	Gln	Lys	Thr	His	Thr	Thr	Phe	Lys	Cys	Leu	Ser	Cys	Val	Lys	Val		
	90				95					100					105		
cta	aaa	aat	gtt	aag	ttt	atg	aat	cac	gtg	aag	cat	cat	ttg	gaa	ttt		446
Leu	Lys	Asn	Val	Lys	Phe	Met	Asn	His	Val	Lys	His	His	Leu	Glu	Phe		
				110					115					120			
gag	aag	cag	agg	aac	gac	agc	tgg	gaa	aac	cac	acc	acc	tgc	cag	cac		494
Glu	Lys	Gln	Arg	Asn	Asp	Ser	Trp	Glu	Asn	His	Thr	Thr	Cys	Gln	His		
			125					130					135				
tgc	cac	cgg	agt	ctt	ccc	act	ccc	ttc	cag	cta	cag	tgt	cac	atc	gaa		542
Cys	His	Arg	Ser	Leu	Pro	Thr	Pro	Phe	Gln	Leu	Gln	Cys	His	Ile	Glu		
		140					145					150					
aat	gtc	cac	act	gcc	cag	gag	ccc	tct	act	gtc	tgt	aaa	atc	tgt	gaa		590
Asn	Val	His	Thr	Ala	Gln	Glu	Pro	Ser	Thr	Val	Cys	Lys	Ile	Cys	Glu		
	155					160					165						
ttg	tca	ttt	gaa	aca	gat	cag	gtc	ctc	tta	caa	cac	atg	aag	gac	cat		638
Leu	Ser	Phe	Glu	Thr	Asp	Gln	Val	Leu	Leu	Gln	His	Met	Lys	Asp	His		
	170				175					180					185		
cat	aag	cct	ggc	gaa	atg	ccc	tat	gtg	tgc	cag	gtt	tgc	cat	tat	aga		686
His	Lys	Pro	Gly	Glu	Met	Pro	Tyr	Val	Cys	Gln	Val	Cys	His	Tyr	Arg		
				190					195					200			
tcg	tcg	gtc	ttt	gct	gat	gta	gaa	aca	cat	ttt	aga	acg	tgc	cat	gaa		734
Ser	Ser	Val	Phe	Ala	Asp	Val	Glu	Thr	His	Phe	Arg	Thr	Cys	His	Glu		
			205					210					215				
aac	aca	aag	aat	ttg	ctt	tgt	ccc	ttt	tgt	ctc	aaa	att	ttc	aaa	aca		782
Asn	Thr	Lys	Asn	Leu	Leu	Cys	Pro	Phe	Cys	Leu	Lys	Ile	Phe	Lys	Thr		
		220					225					230					
gca	aca	cca	tac	atg	tgt	cat	tat	agg	ggc	cac	tgg	gga	aag	agt	gca		830
Ala	Thr	Pro	Tyr	Met	Cys	His	Tyr	Arg	Gly	His	Trp	Gly	Lys	Ser	Ala		

235	240	245	
cac cag tgt tcc aag tgc cgg cta cag ttt tta act ttc aag gag aaa			878
His Gln Cys Ser Lys Cys Arg Leu Gln Phe Leu Thr Phe Lys Glu Lys			
250	255	260	265
atg gag cac aag acc cag tgt cat caa atg ttt aag aag cct aag caa			926
Met Glu His Lys Thr Gln Cys His Gln Met Phe Lys Lys Pro Lys Gln			
	270	275	280
cta gaa gga tta cct cct gaa aca aaa gtt act att caa gtg tca ctg			974
Leu Glu Gly Leu Pro Pro Glu Thr Lys Val Thr Ile Gln Val Ser Leu			
	285	290	295
gaa cct ctt cag cca gga tca gtg gat gta gca tcc ata act gtg agc			1022
Glu Pro Leu Gln Pro Gly Ser Val Asp Val Ala Ser Ile Thr Val Ser			
	300	305	310
aca tct gac tct gaa cca tca ctg ccc agg tct aaa agc aaa att tca			1070
Thr Ser Asp Ser Glu Pro Ser Leu Pro Arg Ser Lys Ser Lys Ile Ser			
	315	320	325
aaa aag tcc cat taa ttctagtttc agtaaatcta aagcaagtat ttcaaacc			1125
Lys Lys Ser His *			
330			
attaaaaaac ctcataaaac aaaaaataca aaccatacat tattcagtag caccaaaaat			1185
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		atg cct tct	114
		Met Pro Ser	
		1	
gca tcc tgt gat aca cta ctg gat gac atc gaa gat atc gtg tct cag			162
Ala Ser Cys Asp Thr Leu Leu Asp Asp Ile Glu Asp Ile Val Ser Gln			
5	10	15	
gaa gat tca aaa cca caa gat agg cat ttt gta aga aag gat gtt gtc			210
Glu Asp Ser Lys Pro Gln Asp Arg His Phe Val Arg Lys Asp Val Val			

20	25	30	35	
ccg aag gta cga agg cga aat acc caa aaa tat ttg caa gag gaa gaa				258
Pro Lys Val Arg Arg Arg Asn Thr Gln Lys Tyr Leu Gln Glu Glu Glu	40	45	50	
aac agt cca cca agt gac agc act att cca ggc ata cag aaa att tgg				306
Asn Ser Pro Pro Ser Asp Ser Thr Ile Pro Gly Ile Gln Lys Ile Trp	55	60	65	
ata cga aca tgg ggt tgt tct cat aat aat tca gat gga gaa tat atg				354
Ile Arg Thr Trp Gly Cys Ser His Asn Asn Ser Asp Gly Glu Tyr Met	70	75	80	
gct gga cag cta gct gct tat ggc tat aaa att aca gaa aat gca tcc				402
Ala Gly Gln Leu Ala Ala Tyr Gly Tyr Lys Ile Thr Glu Asn Ala Ser	85	90	95	
gat gca gat tta tgg ctc ctg aac agt tgc act gta aaa aac cca gct				450
Asp Ala Asp Leu Trp Leu Leu Asn Ser Cys Thr Val Lys Asn Pro Ala	100	105	110	115
gaa gac cac ttt aga aac tca att aaa aaa gct caa gag gag aac aag				498
Glu Asp His Phe Arg Asn Ser Ile Lys Lys Ala Gln Glu Glu Asn Lys	120	125	130	
aaa atc gta ctg gct gga tgc gtt cct caa gcc cag cct cgc cag gac				546
Lys Ile Val Leu Ala Gly Cys Val Pro Gln Ala Gln Pro Arg Gln Asp	135	140	145	
tac ctt aag gga ctg agt atc att ggg gtt cag cag ata gat cgt gtg				594
Tyr Leu Lys Gly Leu Ser Ile Ile Gly Val Gln Gln Ile Asp Arg Val	150	155	160	
gta gaa gtt gtg gag gag aca att aaa ggt cac tct gtg aga ctg ctg				642
Val Glu Val Val Glu Glu Thr Ile Lys Gly His Ser Val Arg Leu Leu	165	170	175	
ggt cag aaa aag gat aat gga agg cgg ctt ggg gga gca cga ttg gat				690
Gly Gln Lys Lys Asp Asn Gly Arg Arg Leu Gly Gly Ala Arg Leu Asp	180	185	190	195
ttg ccg aag att agg aag aat cca ctg ata gaa atc att tcc atc aat				738
Leu Pro Lys Ile Arg Lys Asn Pro Leu Ile Glu Ile Ile Ser Ile Asn	200	205	210	
acc ggg tgt ctc aat gct tgt acc tac tgc aaa act aaa cac gcc aga				786
Thr Gly Cys Leu Asn Ala Cys Thr Tyr Cys Lys Thr Lys His Ala Arg	215	220	225	
gga aat ttg gcc agt tat cca att gat gaa cta gta gat aga gcc aaa				834
Gly Asn Leu Ala Ser Tyr Pro Ile Asp Glu Leu Val Asp Arg Ala Lys	230	235	240	
caa tct ttt caa gag ggt gtt tgt gag ata tgg ttg acc agt gaa gac				882
Gln Ser Phe Gln Glu Gly Val Cys Glu Ile Trp Leu Thr Ser Glu Asp	245	250	255	

acg ggg gct tat ggc aga gat att ggc acc aat ctc ccc aca ctc ctg	930
Thr Gly Ala Tyr Gly Arg Asp Ile Gly Thr Asn Leu Pro Thr Leu Leu	
260 265 270 275	
tgg aaa ctg gtt gaa gtg att cct gag gga gca atg ctg agg ctt ggc	978
Trp Lys Leu Val Glu Val Ile Pro Glu Gly Ala Met Leu Arg Leu Gly	
280 285 290	
atg aca aat ccg ccc tat att tta gag cat ctg gag gaa atg gca aaa	1026
Met Thr Asn Pro Pro Tyr Ile Leu Glu His Leu Glu Glu Met Ala Lys	
295 300 305	
atc ctt aat cac ccc aga gtc tac gct ttt ctg cac ata cca gtc cag	1074
Ile Leu Asn His Pro Arg Val Tyr Ala Phe Leu His Ile Pro Val Gln	
310 315 320	
tct gcc tcc gac agc gta ctc atg gaa atg aaa aga gaa tac tgt gtg	1122
Ser Ala Ser Asp Ser Val Leu Met Glu Met Lys Arg Glu Tyr Cys Val	
325 330 335	
gct gac ttc aaa aga gta gtg gat ttt ctg aaa gag aaa gtt cct gga	1170
Ala Asp Phe Lys Arg Val Val Asp Phe Leu Lys Glu Lys Val Pro Gly	
340 345 350 355	
ata act att gct aca gat att atc tgt ggt ttt cct gga gaa aca gat	1218
Ile Thr Ile Ala Thr Asp Ile Ile Cys Gly Phe Pro Gly Glu Thr Asp	
360 365 370	
cag gat ttt caa gaa aca gtg aaa ctt gtt gaa gag tac aaa ttc cca	1266
Gln Asp Phe Gln Glu Thr Val Lys Leu Val Glu Glu Tyr Lys Phe Pro	
375 380 385	
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Ser Leu Phe Ile Asn Gln Phe Tyr Pro Arg Pro Gly Thr Pro Ala Ala	
390 395 400	
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Lys Met Glu Gln Val Pro Ala Gln Val Lys Lys Gln Arg Thr Lys Asp	
405 410 415	
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Leu Ser Arg Val Phe His Ser Tyr Ser Pro Tyr Asp His Lys Ile Gly	
420 425 430 435	
gaa aga caa caa gtg tta gta aca gaa gaa tct ttt gat tcc aag ttt	1458
Glu Arg Gln Gln Val Leu Val Thr Glu Glu Ser Phe Asp Ser Lys Phe	
440 445 450	
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Tyr Val Ala His Asn Gln Phe Tyr Glu Gln Val Leu Val Pro Lys Asn	
455 460 465	
cct gcg ttc atg ggg aag atg gtt gaa gtg gac atc tat gaa tca ggc	1554
Pro Ala Phe Met Gly Lys Met Val Glu Val Asp Ile Tyr Glu Ser Gly	
470 475 480	

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Lys His Phe Met Lys Gly Gln Pro Val Ser Asp Ala Lys Val Tyr Thr	
485 490 495	
ccc tcc atc agc aaa ccg cta gca aag gga gaa gtc tca ggt ttg aca	1650
Pro Ser Ile Ser Lys Pro Leu Ala Lys Gly Glu Val Ser Gly Leu Thr	
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Lys Asp Phe Arg Asn Gly Leu Gly Asn Gln Leu Ser Ser Gly Ser His	
520 525 530	
acc tct gct gca tct cag tgt gac tca gcg agt tcc aga atg gtg ctg	1746
Thr Ser Ala Ala Ser Gln Cys Asp Ser Ala Ser Ser Arg Met Val Leu	
535 540 545	
ccc atg cca agg cta cat caa gac tgt gcg ctg agg atg tcc gtg ggc	1794
Pro Met Pro Arg Leu His Gln Asp Cys Ala Leu Arg Met Ser Val Gly	
550 555 560	
ttg gct ctg ctg ggt ctt ctt ttt gct ttt ttt gtc aag gtc tat aat	1842
Leu Ala Leu Leu Gly Leu Leu Phe Ala Phe Phe Val Lys Val Tyr Asn	
565 570 575	
tag aata caactaatgg aaacatctat aaagaagaat acattttctaa ttaaaatctt	1899
* 580	
caatgaacag gaaagcgaca tctccattct ccaagggcaa taattttgtac tggatcatgct	1959
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gaagaatttt ctatctttta taaacttttt ctttggtttt tttttccaga tggagtttcg	2259
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ataccaccat gcccaactaa ttttttaatt ttttgtagag atgagtgtca ctatgttgcc	2439
caggcttgcc tggaactcct agcctcaagc agtcttcttg cctcagcctc ccaaagtgt	2499
gggattacag gcgtgagcca ctccaccag ccagattaa atgtttttat ttctacctgc	2559
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actaagcaaa aaaaaaaaaa	2638

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (250)..(1275)

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tggctggagg ggagggtagt gagatgggcg gccatctgct ggtagacatg cgggaggact      180
ttccggggca gtgggtttcc agccccaca tgcccctcag tggggccctg tgccctagag      240
tacaccaag   atg aag act gca gat cac ttc tgg acc gat ccc tcg gct      288
              Met Lys Thr Ala Asp His Phe Trp Thr Asp Pro Ser Ala
              1               5               10
gac gaa ctt gtc cag agg cac cgc atc cac agc tcc cac gtg cgg cag      336
Asp Glu Leu Val Gln Arg His Arg Ile His Ser Ser His Val Arg Gln
   15               20               25
gac tcg ccc acc aag cgt cct gcc ctc tgt atc cag aag agg cat tcc      384
Asp Ser Pro Thr Lys Arg Pro Ala Leu Cys Ile Gln Lys Arg His Ser
   30               35               40               45
agt ggc agc atg gat gac cgg cca tcc ctc tct gcc cgc gac tac gtg      432
Ser Gly Ser Met Asp Asp Arg Pro Ser Leu Ser Ala Arg Asp Tyr Val
              50               55               60
gag tcc ctg cat cag aac tcc cgt gcc acc ctt ctc tat ggc aaa aac      480
Glu Ser Leu His Gln Asn Ser Arg Ala Thr Leu Leu Tyr Gly Lys Asn
              65               70               75
aac gtt ctt gtt cag ccg agg gac gac atg gag gct gtg cca ggg tac      528
Asn Val Leu Val Gln Pro Arg Asp Asp Met Glu Ala Val Pro Gly Tyr
              80               85               90
ctg tcc ctg cac cag acg gct gac gtc atg acc ttg aag tgg aca ccc      576
Leu Ser Leu His Gln Thr Ala Asp Val Met Thr Leu Lys Trp Thr Pro
              95               100              105
aac cag ctg atg aac ggg tct gtg ggg gac ctg gac tat gag aag agc      624
Asn Gln Leu Met Asn Gly Ser Val Gly Asp Leu Asp Tyr Glu Lys Ser
   110               115               120               125
gtc tac tgg gac tat gcc atg acc atc cgc ttg gag gag att gtc tac      672
Val Tyr Trp Asp Tyr Ala Met Thr Ile Arg Leu Glu Glu Ile Val Tyr
              130               135               140
ctg cac tgc cac cag caa gtt gac agc ggc ggg aca gtg gta ttg gtc      720
Leu His Cys His Gln Gln Val Asp Ser Gly Gly Thr Val Val Leu Val
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agc Ser	cag Gln	gac Asp	ggg Gly	atc Ile	cag Gln	agg Arg	ccg Pro	ccc Pro	ttc Phe	cgc Arg	ttc Phe	ccc Pro	aag Lys	ggc Gly	ggg Gly	768
160 165 170																
cac His	ctc Leu	ctg Leu	cag Gln	ttc Phe	ctc Leu	tcg Ser	tgc Cys	ctg Leu	gag Glu	aat Asn	ggg Gly	ctg Leu	ctc Leu	cca Pro	cat His	816
175 180 185																
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190 195 200 205																
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210 215 220																
tct Ser	tca Ser	gac Asp	aaa Lys	gat Asp	gat Asp	gat Asp	gag Glu	gcc Ala	acg Thr	gat Asp	tat Tyr	gtg Val	ttc Phe	agg Arg	atc Ile	960
225 230 235																
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240 245 250																
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255 260 265																
ggc Gly	cgg Arg	tcc Ser	atg Met	ctg Leu	gtg Val	gtg Val	gcc Ala	aga Arg	ggg Gly	agt Ser	cag Gln	tgg Trp	gag Glu	cca Pro	gcc Ala	1104
270 275 280 285																
aga Arg	tgg Trp	gac Asp	act Thr	act Thr	ctc Leu	ccc Pro	acg Thr	cca Pro	agc Ser	ccg Pro	aag Lys	gag Glu	cag Gln	ccc Pro	ccc Pro	1152
290 295 300																
agt Ser	aat Asn	gtc Val	tgg Trp	gat Asp	ctc Leu	ccc Pro	gtc Val	ccc Pro	agg Arg	ggc Gly	tgg Trp	gtg Val	cca Pro	gcc Ala	acc Thr	1200
305 310 315																
tct Ser	gcc Ala	atg Met	ttg Leu	tca Ser	att Ile	gag Glu	ttc Phe	tgg Trp	tcc Ser	caa Gln	ggg Gly	aga Arg	tgg Trp	agg Arg	cag Gln	1248
320 325 330																
gaa Glu	ggg Gly	aga Arg	tgg Trp	agg Arg	cag Gln	agg Arg	gat Asp	tga *	tgccc	tcctgctgtc	cagcctccac					1300
335 340																
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<210>	341
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<212>	DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (101)..(637)

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aaggagcgtc acacgattaa gtatcgtgtc acataatagg atg aca aag ttt tta 115
Met Thr Lys Phe Leu
1 5

att gtt tca gat aca cat ggt gat cgt gag atc att gct gat att ttt 163
Ile Val Ser Asp Thr His Gly Asp Arg Glu Ile Ile Ala Asp Ile Phe
10 15 20

gac aaa tgg cgg gat agc gtt gcc ggc att ttt tac aat ggg gat tct 211
Asp Lys Trp Arg Asp Ser Val Ala Gly Ile Phe Tyr Asn Gly Asp Ser
25 30 35

gaa tta gcg gct gat gac aca gta ttt gat ggc gta tcc act gtg att 259
Glu Leu Ala Ala Asp Asp Thr Val Phe Asp Gly Val Ser Thr Val Ile
40 45 50

ggc aat atg gat gat gat cct gat ttc gtg gcc gca agg gcg aca acg 307
Gly Asn Met Asp Asp Asp Pro Asp Phe Val Ala Ala Arg Ala Thr Thr
55 60 65

att gat ggg att act ttt ttc caa acg cac gga cat ctc tat gac gcg 355
Ile Asp Gly Ile Thr Phe Phe Gln Thr His Gly His Leu Tyr Asp Ala
70 75 80 85

acc caa ttt aac gct tgg gcg aac cta aaa tta atg gcc gtg gca gca 403
Thr Gln Phe Asn Ala Trp Ala Asn Leu Lys Leu Met Ala Val Ala Ala
90 95 100

cag gaa gct aac gca cag gtc gcc ctc ttt ggg cat acc cat ctg gaa 451
Gln Glu Ala Asn Ala Gln Val Ala Leu Phe Gly His Thr His Leu Glu
105 110 115

ggg gcg gtt gtg ttt gat gat atc ttg ttt att aat cca ggt tca atc 499
Gly Ala Val Val Phe Asp Asp Ile Leu Phe Ile Asn Pro Gly Ser Ile
120 125 130

cgg ctg cct aaa ggg cca cat gcc aac tta ggt ggt act tat gct gtg 547
Arg Leu Pro Lys Gly Pro His Ala Asn Leu Gly Gly Thr Tyr Ala Val
135 140 145

ttg gat gtg acg gag acg agc tat gac gtg aga ttt tat aat cgt cag 595
Leu Asp Val Thr Glu Thr Ser Tyr Asp Val Arg Phe Tyr Asn Arg Gln
150 155 160 165

cat caa cca ttg cca caa ctc acg gta cag gtc gca cgt taa gtgaccc 644
His Gln Pro Leu Pro Gln Leu Thr Val Gln Val Ala Arg *
170 175

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caatttaatc aatggatatg 723

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (364)..(543)

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tcctgggacc aagaccagga aatctaacca ataagcaatg gtaacagtga ctcaagtgtc 180
agtccgccct cagtggcccg agtccgaggt gggcatcatg gcaccagttt acatctcgga 240
aagggaggct cagagaggct aagtcacttg cctaagggtca cccagggact gcttagctgg 300
ctaggatgag aaccagcctg ctccaacgcc cctcgtgga acagttgcga gcctaggaat 360
taa atg ttc cct ccc cca ggc tat gcc aat gag gtg ggc gag gct ttc 408
Met Phe Pro Pro Pro Gly Tyr Ala Asn Glu Val Gly Glu Ala Phe
1 5 10 15
cgc tct ctt gtg cca gcg gcg gtg gtg tgg ctg agc tat ggc gtg gcc 456
Arg Ser Leu Val Pro Ala Ala Val Val Trp Leu Ser Tyr Gly Val Ala
20 25 30
agc tcc tac gtg ctg gcg gat gcc att gac aaa ggc aag aag gct gga 504
Ser Ser Tyr Val Leu Ala Asp Ala Ile Asp Lys Gly Lys Lys Ala Gly
35 40 45
gag gtg agt gtt agc cta ttt tcc aac ccc caa ccc tag ctctcctctt 553
Glu Val Ser Val Ser Leu Phe Ser Asn Pro Gln Pro *
50 55 60
gtgtggctca gtccacagcc tggcatgtga taaagtcctt gtgggacact ccagtccta 613
caacttgctt agtgcagtcc ataa 637

<210> 343
<211> 998
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> (7)..(399)

<400> 343

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	1 5 10	
aag ttc atg cct att ctg ggg ttt ggc acc tct gtt gct agg aag gtt	96	
Lys Phe Met Pro Ile Leu Gly Phe Gly Thr Ser Val Ala Arg Lys Val		
15 20 25 30		
gct atg agt aat gta gaa gaa gcc gtc cag gta gca att gat gta ggc	144	
Ala Met Ser Asn Val Glu Glu Ala Val Gln Val Ala Ile Asp Val Gly		
35 40 45		
tac cgc cat att gac tca gct tat aca cac ctg aat gaa gaa ggc atc	192	
Tyr Arg His Ile Asp Ser Ala Tyr Thr His Leu Asn Glu Glu Gly Ile		
50 55 60		
ggg cag gcc atc cga aag aag att gcc aac ggc act gtg aag aga aaa	240	
Gly Gln Ala Ile Arg Lys Lys Ile Ala Asn Gly Thr Val Lys Arg Lys		
65 70 75		
gat ata ttc tat acc aca aag gtg tgg ggc acc ttt tcc cgc cca gaa	288	
Asp Ile Phe Tyr Thr Thr Lys Val Trp Gly Thr Phe Ser Arg Pro Glu		
80 85 90		
ttg gtc caa aga ggc ctt gaa atg tca ctg aag aaa ctt cag ctg agc	336	
Leu Val Gln Arg Gly Leu Glu Met Ser Leu Lys Lys Leu Gln Leu Ser		
95 100 105 110		
tac atg gat ctt tac ctt ttt cat ttc cca gta cct ttg cag cct ggg	384	
Tyr Met Asp Leu Tyr Leu Phe His Phe Pro Val Pro Leu Gln Pro Gly		
115 120 125		
agg agc ttt tgc tga cggatgcaca gggaaagatc atgtttgaca cagtgggtct	439	
Arg Ser Phe Cys *		
130		
ctgcagcaca tgggagagtt ttactcctgt tgccaaggct ggagtacagt ggcacgatct	499	
cggctcactg caacctccgc ctcccagggt caagcatgta cctctgcctc ccacatagct	559	
gggaatacag gtggaatatc acccttacct caaccaaagc aaactcctgg agtactgtaa	619	
gtccaaggac attgtcatga ctgcatattc tgcccttgggg tctgactcag acaaagactg	679	
gtaatcatct tcataaagtt attttgttta ttttttttag gtgggggtct cattctgtca	739	
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gcctggctaa ttgtttatct tcatttttgt agagacaggg tctcactacg ttacccaagc	919	

cagtcttgaa ttcttgggct caagtgatcc tcccaccttg gcctcccaaa gtgctgggat 979
tagaggtgta agccacggt 998

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<222> (188)..(376)

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actgctgctg tggagctcag catcaagtac ttccaggaga agcttcagca ggacctagag 180
gcagagc atg gta gag gta gag gat aca gcc ctc ata cca ccg tgc tgt 229
Met Val Glu Val Glu Asp Thr Ala Leu Ile Pro Pro Cys Cys
1 5 10
atg tcc atc ttt caa gtc ctg gtg gtg ccc gca gag ttt gaa ggg aag 277
Met Ser Ile Phe Gln Val Leu Val Val Pro Ala Glu Phe Glu Gly Lys
15 20 25 30
cca ctg ctt cag aga tac cag gtg gta aat gca tgc cta gtg gaa gtg 325
Pro Leu Leu Gln Arg Tyr Gln Val Val Asn Ala Cys Leu Val Glu Val
35 40 45
tgc tcc tct gca tct atg cct ttg agc aga aag cct ttg agt ccc aat 373
Cys Ser Ser Ala Ser Met Pro Leu Ser Arg Lys Pro Leu Ser Pro Asn
50 55 60
tag tggg cccatgagtg gccaaaatga gggactggga cctgtatagc cgttaaacta 430
*
taaatacagg ccaaaaagga aagataaatt ataagtttaa agaaaatg 478

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<212> DNA
<213> Homo sapiens

<220>
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<222> (201)..(368)


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tctcctgtgt cacctctctt gtgtccacag tctaacccat ctcttcattt ccctcaacct      180
caggtggagc ctccacaaaa      atg cag att ttt cca aaa atc ctt aca ggg      230
                        Met Gln Ile Phe Pro Lys Ile Leu Thr Gly
                        1             5             10
acg atc atc acc cta gag gtt gaa ccc ttg gat aca aca gaa aaa tgt      278
Thr Ile Ile Thr Leu Glu Val Glu Pro Leu Asp Thr Thr Glu Lys Cys
                        15             20             25
aaa ggc caa tat cag gat aag gaa cga att cct cct gat cag caa aga      326
Lys Gly Gln Tyr Gln Asp Lys Glu Arg Ile Pro Pro Asp Gln Gln Arg
                        30             35             40
caa gtg act gga agc tgg caa gta act gga aga tgg aca taa ctttctc      375
Gln Val Thr Gly Ser Trp Gln Val Thr Gly Arg Trp Thr *
                        45             50             55
tgactacaac attcaaaagg aatttactct ttttatgttg tgttgagact tcatggtagt      435
gctaaaacta ggaagaaatc ttac      459

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<210> 346
<211> 1867
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (9)..(1835)

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      1             5             10
ttg cca aaa tac cta ttt gat ctt ccc ctt aaa gtt ttg gtc gtc agt      98
Leu Pro Lys Tyr Leu Phe Asp Leu Pro Leu Lys Val Leu Val Val Ser
      15             20             25             30
aat aat aaa ctg gta tcc att cca gaa gaa att ggg aag tta aaa gat      146
Asn Asn Lys Leu Val Ser Ile Pro Glu Glu Ile Gly Lys Leu Lys Asp
      35             40             45
tta atg gaa ttg gat att agc tgc aat gag att caa gtc ctt ccc caa      194
Leu Met Glu Leu Asp Ile Ser Cys Asn Glu Ile Gln Val Leu Pro Gln
      50             55             60
caa atg gga aaa tta cat tca ctt aga gag cta aat ata aga aga aat      242

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	290	295	300	
	gca gag gaa gag gat gat gat	ttg aag gaa gta act gat	ttg agg aaa	962
	Ala Glu Glu Glu Asp Asp Asp	Leu Lys Glu Val Thr Asp	Leu Arg Lys	
	305	310	315	
	ata gct gct cag tta ttg cag	caa gaa cag aag aac agg att	ctt aat	1010
	Ile Ala Ala Gln Leu Leu Gln	Gln Glu Gln Lys Asn Arg	Ile Leu Asn	
	320	325	330	
	cat tca act tct gtg atg aga	aac aag cca aaa caa act	gtg gaa tgt	1058
	His Ser Thr Ser Val Met Arg	Asn Lys Pro Lys Gln Thr	Val Glu Cys	
	335	340	345	350
	gaa aag agt gtc tca gca gat	gaa gtt aat tca cca tta	tca ccc ctc	1106
	Glu Lys Ser Val Ser Ala Asp	Glu Val Asn Ser Pro Leu	Ser Pro Leu	
	355	360	365	
	acc tgg cag ccc tta gaa aat	cag aag gat caa ata gat	gaa caa ccg	1154
	Thr Trp Gln Pro Leu Glu Asn	Gln Lys Asp Gln Ile Asp	Glu Gln Pro	
	370	375	380	
	tgg cca gaa tct cac cct ata	atc tgg cag agt gaa gaa	agg agg cgg	1202
	Trp Pro Glu Ser His Pro Ile	Ile Trp Gln Ser Glu Glu	Arg Arg Arg	
	385	390	395	
	agc aaa cag att aga aaa gaa	tat ttc aag tat aaa tca	atg agg aag	1250
	Ser Lys Gln Ile Arg Lys Glu	Tyr Phe Lys Tyr Lys Ser	Met Arg Lys	
	400	405	410	
	agt tca agt ggc aat gaa aat	gat gag caa gac agt gat	aat gct aat	1298
	Ser Ser Ser Gly Asn Glu Asn	Asp Glu Gln Asp Ser Asp	Asn Ala Asn	
	415	420	425	430
	atg tca aca caa tct cca gta	tca tct gag gaa tat gac	aga act gat	1346
	Met Ser Thr Gln Ser Pro Val	Ser Ser Glu Glu Tyr Asp	Arg Thr Asp	
	435	440	445	
	ggc ttt tca cac agt ccc ttt	ggc ttg aag cct aga tca	gct ttt agc	1394
	Gly Phe Ser His Ser Pro Phe	Gly Leu Lys Pro Arg Ser	Ala Phe Ser	
	450	455	460	
	cgc tca tct cgc caa gaa tat	ggg gca gca gat cca gga	ttt aca atg	1442
	Arg Ser Ser Arg Gln Glu Tyr	Gly Ala Ala Asp Pro Gly	Phe Thr Met	
	465	470	475	
	aga aga aag atg gaa cat tta	cgg gaa gag cga gag caa	ata cga caa	1490
	Arg Arg Lys Met Glu His Leu	Arg Glu Glu Arg Glu Gln	Ile Arg Gln	
	480	485	490	
	ctt cgc aac aat ctt gaa tcc	agg tta aaa gta att ttg	cct gat gac	1538
	Leu Arg Asn Asn Leu Glu Ser	Arg Leu Lys Val Ile Leu	Pro Asp Asp	
	495	500	505	510
	att gga gct gca ctg atg gat	ggg gtt gtt ctt tgc cat	tta gcc aat	1586
	Ile Gly Ala Ala Leu Met Asp	Gly Val Val Leu Cys His	Leu Ala Asn	
	515	520	525	

cat ata agg cca cgt tct gtt gct agt att cat gta cca tca cca gca	1634
His Ile Arg Pro Arg Ser Val Ala Ser Ile His Val Pro Ser Pro Ala	
530 535 540	
gtg ccc aaa ctg agc atg gca aaa tgt cga aga aat gta gaa aat ttt	1682
Val Pro Lys Leu Ser Met Ala Lys Cys Arg Arg Asn Val Glu Asn Phe	
545 550 555	
ctt gat gct tgt aaa aag ttg ggt gtc tca cag gaa aga ctt tgt ttg	1730
Leu Asp Ala Cys Lys Lys Leu Gly Val Ser Gln Glu Arg Leu Cys Leu	
560 565 570	
cct cat cat att ttg gaa gaa cga gga ctt gtg aaa gtt ggt gtc aca	1778
Pro His His Ile Leu Glu Glu Arg Gly Leu Val Lys Val Gly Val Thr	
575 580 585 590	
gtt cag gcg ctc ctt gaa tta cca aca acc aag gca tct cag ctt tct	1826
Val Gln Ala Leu Leu Glu Leu Pro Thr Thr Lys Ala Ser Gln Leu Ser	
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Val Ala *	

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tactgtcatt ca atg tgg att gct tcc tta tgt ttc att att ttg gat	168
Met Trp Ile Ala Ser Leu Cys Phe Ile Ile Leu Asp	
1 5 10	
tgt gag ctc atc ttt tgt agg gtg tta gct aca gaa atc cta tgc tgc	216
Cys Glu Leu Ile Phe Cys Arg Val Leu Ala Thr Glu Ile Leu Cys Cys	
15 20 25	
agg gtt gag att tgt ccc tat ttg ctt ctg tat tac tgc cta agg acc	264
Arg Val Glu Ile Cys Pro Tyr Leu Leu Leu Tyr Tyr Cys Leu Arg Thr	
30 35 40	
aac ttt gct cat tta aaa tat att tat ata agc tca aag att aaa gct	312
Asn Phe Ala His Leu Lys Tyr Ile Tyr Ile Ser Ser Lys Ile Lys Ala	

45	50	55	60	
gac tgt ggg gag gtc tat ggc taa aaattttcaa gggagatttc ttccccctaa				366
Asp Cys Gly Glu Val Tyr Gly *				
	65			
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tatactcttt cactgcaagc atggctcttc gagggctctg gctctatgac gaagtcttca				486
gttccaaatc ttcatcttgt gccagcctaa cgcctttgtt t				527
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gcatacatct cagtggcatg agcattgtgg aatatecttt cctaggcaca tttgtccact				300
aagggaacag cctcagaaac tggtagacga atgggtgaga tgagatcctg gagagagaac				360
acagccatcc cctatagaaa ggcacagctt ttgggcttct ctggcctga			atg cct	415
			Met Pro	
			1	
tct ggg gta ttt cca tat gca aca gcc cag agt cat agc ctt ggg caa				463
Ser Gly Val Phe Pro Tyr Ala Thr Ala Gln Ser His Ser Leu Gly Gln				
5 10 15				
cca cac ata gag gtt tcc ttc tca ctt cag aca cat aca tca ctt tca				511
Pro His Ile Glu Val Ser Phe Ser Leu Gln Thr His Thr Ser Leu Ser				
20 25 30				
cac cac ttg ggg atg gaa ata cct aca aga gtg aag gtc aag ggc cct				559
His His Leu Gly Met Glu Ile Pro Thr Arg Val Lys Val Lys Gly Pro				
35 40 45 50				
ccc cag gca tct cat tca tta ctc agc ttc ctt cct gac caa gtc tgc				607
Pro Gln Ala Ser His Ser Leu Leu Ser Phe Leu Pro Asp Gln Val Cys				
55 60 65				

caa cca atg gcc agc tat gcg cct cat cct cat tgc ttc tgc ctc cac	655
Gln Pro Met Ala Ser Tyr Ala Pro His Pro His Cys Phe Cys Leu His	
70 75 80	
gta aat gaa acc aaa ggc ctc agc ata tcc tgg gag gac tgg ggg ctg	703
Val Asn Glu Thr Lys Gly Leu Ser Ile Ser Trp Glu Asp Trp Gly Leu	
85 90 95	
tta cct aat ggt cct ctc tgt ccc att ata ggt gca agg cac ccc atc	751
Leu Pro Asn Gly Pro Leu Cys Pro Ile Ile Gly Ala Arg His Pro Ile	
100 105 110	
cac aca ttt gca cca cta ctc caa gat agt att ttt ctt ttc aca caa	799
His Thr Phe Ala Pro Leu Leu Gln Asp Ser Ile Phe Leu Phe Thr Gln	
115 120 125 130	
tct ctt tac agc aga atc cag agt tgg gtt gta gtt tac ctt cct gga	847
Ser Leu Tyr Ser Arg Ile Gln Ser Trp Val Val Val Tyr Leu Pro Gly	
135 140 145	
aag ctc att atc ttt gtt tga at taacatttca gcatggaact aactgggcgg	900
Lys Leu Ile Ile Phe Val *	
150	
aggaaggatc gttatacgtc ttcagaaagt tctcattgcc ccagctgcct agtactatac	960
aagaagctct actttgatgg cagatctaag aaggctatag gcctttgttt gtaggaagca	1020
gtgtcattac attcaagctt cacttctctg attggcttcc aaccactggg attcaaagag	1080
aatccaaggt tctgcctatg tctgatgaca taaggaaaac ttggcttcct ctgctcaagg	1140
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aagcaggcaa agagtactat ccacatggca ggcaggtggc tttgtgtctg gaaagctttg	1560
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aggaaacatt ctgatcagac cttgggaaaa gctggtgccg agagaggag aggccaggtg	1860
tccccccacc caactggcac tgattctcag ccccttcctc ttacttctgt tggcttcaag	1920

gagacctgcc cttgatgtgt gttgctgctg aagcaccctc ccagccagtg agttggacat 1980
atgcagcagg cactttgatg tccaggaagt acactgggtac atgacaggag caagggtcag 2040
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ctctaaatgg ta 2112

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cag gcg gtg cag gcg gtt cat ctc gag tct gac gct ttc ctc gtt tgt 99
Gln Ala Val Gln Ala Val His Leu Glu Ser Asp Ala Phe Leu Val Cys
15 20 25
ctc aac cac gct ctg agc aca gag aag gag gaa gta atg ggg ctg tgc 147
Leu Asn His Ala Leu Ser Thr Glu Lys Glu Glu Val Met Gly Leu Cys
30 35 40
ata ggg gag ttg aac gat gat aca agg agt gac tcc aaa ttt gca tat 195
Ile Gly Glu Leu Asn Asp Asp Thr Arg Ser Asp Ser Lys Phe Ala Tyr
45 50 55
act gga act gaa atg cgc aca gtt gct gaa aag gtt gat gcc gtc aga 243
Thr Gly Thr Glu Met Arg Thr Val Ala Glu Lys Val Asp Ala Val Arg
60 65 70 75
att gtt cac att cat tct gtc atc atc tta cga cgt tct gat aag agg 291
Ile Val His Ile His Ser Val Ile Ile Leu Arg Arg Ser Asp Lys Arg
80 85 90
aag gac cga gta gaa att tct cca gag cag ctg tct gca gct tca aca 339
Lys Asp Arg Val Glu Ile Ser Pro Glu Gln Leu Ser Ala Ala Ser Thr
95 100 105
gag gca gag agg ttg gct gaa ctg aca ggc cgc ccc atg aga gtt gtg 387
Glu Ala Glu Arg Leu Ala Glu Leu Thr Gly Arg Pro Met Arg Val Val

110	115	120	
ggc tgg tat cat tcc cat cct cat ata act gtt tgg cct tca cat gtt			435
Gly Trp Tyr His Ser His Pro His Ile Thr Val Trp Pro Ser His Val			
125	130	135	
gat gtt cgc aca caa gcc atg tac cag atg atg gat caa ggc ttt gta			483
Asp Val Arg Thr Gln Ala Met Tyr Gln Met Met Asp Gln Gly Phe Val			
140	145	150	155
gga ctt att ttt tcc tgt ttc ata gaa gat aag aac acg aag act ggc			531
Gly Leu Ile Phe Ser Cys Phe Ile Glu Asp Lys Asn Thr Lys Thr Gly			
	160	165	170
cgg gta ctc tac act tgc ttc caa tcc ata cag gcc caa aag agt tca			579
Arg Val Leu Tyr Thr Cys Phe Gln Ser Ile Gln Ala Gln Lys Ser Ser			
	175	180	185
gag tcc ctt cat ggt cca cga gac ttc tgg agc tcc agc cag cac atc			627
Glu Ser Leu His Gly Pro Arg Asp Phe Trp Ser Ser Ser Gln His Ile			
	190	195	200
tcc att gag ggc cag aag gaa gag gaa agg tat gag aga atc gaa atc			675
Ser Ile Glu Gly Gln Lys Glu Glu Glu Arg Tyr Glu Arg Ile Glu Ile			
	205	210	215
cca atc cat att gta cct cat gtc act atc tgg aaa gtg tgc ctt gaa			723
Pro Ile His Ile Val Pro His Val Thr Ile Trp Lys Val Cys Leu Glu			
	220	225	230
tca gca gta gag ctg ccc aag atc ctg tgc cag gag gag cag gat gcg			771
Ser Ala Val Glu Leu Pro Lys Ile Leu Cys Gln Glu Glu Gln Asp Ala			
	240	245	250
tat agg agg atc cac agc ctt aca cat ctg gac tca gta acc aag atc			819
Tyr Arg Arg Ile His Ser Leu Thr His Leu Asp Ser Val Thr Lys Ile			
	255	260	265
cat aat ggc tca gtg ttt acc aag aat ctg tgc agt cag atg tcg gca			867
His Asn Gly Ser Val Phe Thr Lys Asn Leu Cys Ser Gln Met Ser Ala			
	270	275	280
gtc agc ggg cct ctc cta cag tgg ttg gag gac aga ctg gag caa aac			915
Val Ser Gly Pro Leu Leu Gln Trp Leu Glu Asp Arg Leu Glu Gln Asn			
	285	290	295
caa cag cat ttg cag gaa tta caa caa gaa aag gaa gag ctt atg caa			963
Gln Gln His Leu Gln Glu Leu Gln Gln Glu Lys Glu Glu Leu Met Gln			
	300	305	310
gaa ctt tct tct cta gaa taa at caggagacaa aatgggggaaa gatgaaaata			1016
Glu Leu Ser Ser Leu Glu *			
	320		
tccagtgtaa agttacttaa gctaaatcaa tttcaaagaa gaaaaacttg gaggactcat			1076
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aggaacagac acatacgtca atggaacaga tgagagaacc cagaaataaa cccatataaa 1196
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tgacaaatta tgctagagca attagacacc catggcgagg agaaaaaaga acctctactt 1316
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tctgagccga tgtaagagtt cactc  atg ttt gca ccc gcg gtg atg cgt gct 172
                               Met Phe Ala Pro Ala Val Met Arg Ala
                               1           5

ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg atg gat 220
Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Met Asp
 10           15           20           25

cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct tta gag tcg 268
Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu Ser
           30           35           40

gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg aag aat att 316
Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn Ile
           45           50           55

cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa gga aga aat 364
Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg Asn
           60           65           70

cca gaa agc ctt aag act aag aca act tga c tctgctgatt cttttttcct 415
Pro Glu Ser Leu Lys Thr Lys Thr Thr *
 75           80

tttttttttt ttaaaaaaaaa aa 437

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<400> 351

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	1 5	
tgg gtg ctg gtc ctc agt ctg tgg ggg gca gta gta ggt gct caa aac		99
Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn		
10 15 20 25		
atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc		147
Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala		
30 35 40		
ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg		195
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg		
45 50 55		
aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac		243
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp		
60 65 70		
agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc		291
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val		
75 80 85		
ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat		339
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn		
90 95 100 105		
gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct		387
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro		
110 115 120		
ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt		435
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val		
125 130 135		
ccc aat aag gtg ggg aca tgt gtg tca gag gga agc tac cct gca ggg		483
Pro Asn Lys Val Gly Thr Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly		
140 145 150		
act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag		531
Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys		
155 160 165		
gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc		579
Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu		
170 175 180 185		

ttc aca ctg cag tcg gag cta atg gtg acc cca gcc cgg gga gga gat	627
Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp	
190 195 200	
ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac	675
Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His	
205 210 215	
cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg	723
Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val	
220 225 230	
cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta	771
Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val	
235 240 245	
gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc	819
Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro	
250 255 260 265	
tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc	867
Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro	
270 275 280	
ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga	915
Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly	
285 290 295	
acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc	963
Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser	
300 305 310	
cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act	1011
Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr	
315 320 325	
gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg	1059
Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu	
330 335 340 345	
ggg atc ctg gga ggc ctg ggg aca gcc gcc ctg ctc att ggg gtc atc	1107
Gly Ile Leu Gly Gly Leu Gly Thr Ala Ala Leu Leu Ile Gly Val Ile	
350 355 360	
ttg tgg caa agg cgg caa cgc cga gga gag gag agg aag gcc cca gaa	1155
Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu	
365 370 375	
aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa	1203
Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu	
380 385 390	
cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca	1253
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro *	
395 400 405	

gatcccatcc atcagctccc ttttcttttt cccttgaact gttctggcct cagaccaact 1313
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 Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn
 10 15 20 25
 atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc 147
 Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala
 30 35 40
 ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg 195
 Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg
 45 50 55
 aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac 243
 Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp
 60 65 70
 agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc 291
 Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val
 75 80 85
 ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat 339
 Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn
 90 95 100 105
 gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct 387
 Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro
 110 115 120
 ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt 435
 Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val
 125 130 135
 ccc aat aag gta gtg gaa gaa agc agg aga agt aga aaa cgg ccc tgt 483
 Pro Asn Lys Val Val Glu Glu Ser Arg Arg Ser Arg Lys Arg Pro Cys

140	145	150	
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act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys 170 175 180 185			579
gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu 190 195 200			627
ttc aca ctg cag tgc gag cta atg gtg acc cca gcc cgg gga gga gat Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp 205 210 215			675
ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His 220 225 230			723
cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val 235 240 245			771
cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val 250 255 260 265			819
gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro 270 275 280			867
tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro 285 290 295			915
ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly 300 305 310			963
acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser 315 320 325			1011
cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr 330 335 340 345			1059
gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu 350 355 360			1107
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ttg tgg caa agg cgg caa cgc cga gga gag gag agg aag gcc cca gaa	1203
Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu	
380 385 390	
aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa	1251
Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu	
395 400 405	
cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca	1301
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro *	
410 415 420	
gatcccatcc atcagctccc ttttcttttt cccttgaact gttctggcct cagaccaact	1361
ctctcctgta taatctctct cctgtataac cccaccttgc caagctttct tctacaacca	1421
gagcccccca caatgatgat taaacacctg acacatcttg ca	1463

<210> 353
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (10)..(600)

<400> 353	
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Met Val Pro Gly Ser Glu Gly Pro Ala Arg Ala Gly Ser	
1 5 10	
gtg gtg gcc gac gtg gtg ttt gtg att gag ggt acg gcc aac ctg gga	96
Val Val Ala Asp Val Val Phe Val Ile Glu Gly Thr Ala Asn Leu Gly	
15 20 25	
ccc tac ttc gag ggg ctc cgc aag cac tac ctg ctc ccg gcc atc gag	144
Pro Tyr Phe Glu Gly Leu Arg Lys His Tyr Leu Leu Pro Ala Ile Glu	
30 35 40 45	
tat ttt aat ggt ggt cct cct gct gag acg gac ttc ggg gga gac tat	192
Tyr Phe Asn Gly Gly Pro Pro Ala Glu Thr Asp Phe Gly Gly Asp Tyr	
50 55 60	
ggg ggg acc cag tac agc ctc gtg gtg ttc aac aca gtg gac tgc gct	240
Gly Gly Thr Gln Tyr Ser Leu Val Val Phe Asn Thr Val Asp Cys Ala	
65 70 75	
ccc gag tcc tac gta caa tgt cac gct ccc acc agc agc gcc tat gag	288
Pro Glu Ser Tyr Val Gln Cys His Ala Pro Thr Ser Ser Ala Tyr Glu	
80 85 90	
ttt gtc acc tgg ctc gat ggc att aag ttc atg ggc ggg ggt ggt gag	336

Phe	Val	Thr	Trp	Leu	Asp	Gly	Ile	Lys	Phe	Met	Gly	Gly	Gly	Gly	Glu		
95						100					105						
agc	tgc	agc	ctc	atc	gcg	gaa	gga	ctc	agc	aca	gcc	ttg	cag	ctg	ttt	384	
Ser	Cys	Ser	Leu	Ile	Ala	Glu	Gly	Leu	Ser	Thr	Ala	Leu	Gln	Leu	Phe		
110					115				120					125			
gat	gac	ttc	aag	aag	atg	cgc	gag	cag	att	ggc	cag	acg	cac	cgg	gtc	432	
Asp	Asp	Phe	Lys	Lys	Met	Arg	Glu	Gln	Ile	Gly	Gln	Thr	His	Arg	Val		
				130					135					140			
tgc	ctc	ctc	atc	tgc	aac	tca	ccc	cca	tac	ttg	ttg	cct	gct	gtt	gag	480	
Cys	Leu	Leu	Ile	Cys	Asn	Ser	Pro	Pro	Tyr	Leu	Leu	Pro	Ala	Val	Glu		
			145					150					155				
agc	acc	acg	tac	tct	gga	tgc	aca	act	gag	aat	ctt	gtg	cag	cca	gat	528	
Ser	Thr	Thr	Tyr	Ser	Gly	Cys	Thr	Thr	Glu	Asn	Leu	Val	Gln	Pro	Asp		
			160				165					170					
tgg	gga	agc	ggg	gga	tcc	act	tct	cca	ttg	gtg	tct	ccc	cgg	aag	ctg	576	
Trp	Gly	Ser	Gly	Gly	Ser	Thr	Ser	Pro	Leu	Val	Ser	Pro	Arg	Lys	Leu		
	175					180					185						
cct	gcg	ctt	cgg	ctt	cct	ggt	tga	agaaaggcag	ccccccggcc	tgggtggagc						630	
Pro	Ala	Leu	Arg	Leu	Pro	Gly	*										
190					195												
cgctgaggcc	tccgacagat	gttgaggcac	tgaccgaggg	acatggtggt	ggttcgggga											690	
ctcgtgctgc	tgggggggggt	ggtcagccca	gggccttcaa	taaagaagca	gggcctgcca											750	
acagagcgag	cagagacgga	accgcaccac	cgcagagaac	caaagaaagg	cgcaaaaaga											810	
aagcaacaga	ggcaaaaaag	cacacaaacg	cacacgacac	agccgcgcga	caacacgacg											870	
agccaacaca	aaagacgacg	cacaaggcac	gccagaaaag	aggcgagaga	acacaa											926	

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 <213> Homo sapiens

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cttgcgggaa	ttttgcagaa	gtcattgtat	tcaaagaaga	ataagcaaga	aagaaaagaa											120	
ggaaggaaga	gaggtagaca	gatacaag	atg	aaa	tcc	tgt	caa	aaa	atg	gaa						172	
			Met	Lys	Ser	Cys	Gln	Lys	Met	Glu							
			1							5							

gga aaa cca gaa aat gag agt gaa cca aag cat gag gaa gag cca aag 220
 Gly Lys Pro Glu Asn Glu Ser Glu Pro Lys His Glu Glu Glu Pro Lys
 10 15 20

cct gag gaa aag cca gaa gag gag gag aag cta gag gag gag gcc aaa 268
 Pro Glu Glu Lys Pro Glu Glu Glu Glu Lys Leu Glu Glu Glu Ala Lys
 25 30 35 40

gca aaa gga act ttt aga gaa agg ctg att caa tct ctc cag gag ttt 316
 Ala Lys Gly Thr Phe Arg Glu Arg Leu Ile Gln Ser Leu Gln Glu Phe
 45 50 55

aaa gaa gat ata cac aac agg cat tta agc aat gaa gat atg ttt aga 364
 Lys Glu Asp Ile His Asn Arg His Leu Ser Asn Glu Asp Met Phe Arg
 60 65 70

gaa gtg gat gaa ata gat gag ata agg aga gtc aga aac aaa ctt ata 412
 Glu Val Asp Glu Ile Asp Glu Ile Arg Arg Val Arg Asn Lys Leu Ile
 75 80 85

gtg atg cgt tgg aag gta acg aac cct cct acc cca ttt aaa tta gag 460
 Val Met Arg Trp Lys Val Thr Asn Pro Pro Thr Pro Phe Lys Leu Glu
 90 95 100

tac ccg gat ttc tct cat att aca tac cca tag cgctcttata gcagcac 510
 Tyr Pro Asp Phe Ser His Ile Thr Tyr Pro *
 105 110 115

<210> 355
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 <213> Homo sapiens

<220>
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tagaggagta gattaccgag aaaaatatcc catcagtgag gagatttttcg gtatcaccag 60

aaagaccaaa gatcagggct gcttaattgc tgac atg atg gga ctc acc gag 112
 Met Met Gly Leu Thr Glu
 1 5

ggg gtg ttc ctg att ctg tct ggc act cag ttc aca ctg gga att ctg 160
 Gly Val Phe Leu Ile Leu Ser Gly Thr Gln Phe Thr Leu Gly Ile Leu
 10 15 20

gtc aat tgt ttc att gag ttg gtc aat ggt agc agc tgg ttc aag acc 208
 Val Asn Cys Phe Ile Glu Leu Val Asn Gly Ser Ser Trp Phe Lys Thr
 25 30 35

aag aga atg tct ttg tct gac ttc atc atc acc acc ctg gca ctc ttg	256
Lys Arg Met Ser Leu Ser Asp Phe Ile Ile Thr Thr Leu Ala Leu Leu	
40 45 50	
agg atc att ctg ctg tgt att atc ttg act gat agt ttt tta ata gaa	304
Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr Asp Ser Phe Leu Ile Glu	
55 60 65 70	
ttc tct ccc aac aca cat gat tca ggg ata ata atg caa att att gat	352
Phe Ser Pro Asn Thr His Asp Ser Gly Ile Ile Met Gln Ile Ile Asp	
75 80 85	
gtt tcc tgg aca ttt aca aac cat ctg agc att tgg ctt gcc acc tgt	400
Val Ser Trp Thr Phe Thr Asn His Leu Ser Ile Trp Leu Ala Thr Cys	
90 95 100	
ctt ggt gtc ctc tac tgc ctg aaa atc gcc agt ttc tct cac ccc aca	448
Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala Ser Phe Ser His Pro Thr	
105 110 115	
ttc ctc tgg ctc aag tgg aga gtt tct agg gtg atg gta tgg atg ctg	496
Phe Leu Trp Leu Lys Trp Arg Val Ser Arg Val Met Val Trp Met Leu	
120 125 130	
ttg ggt gca ctg ctc tta tcc tgt ggt agt acc gca tct ctg atc aat	544
Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser Thr Ala Ser Leu Ile Asn	
135 140 145 150	
gag ttt aag ctc tat tct gtc ttt agg gga att gag gcc acc agg aat	592
Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly Ile Glu Ala Thr Arg Asn	
155 160 165	
gtg act gaa cac ttc aga aag aag agg agt gag tat tat ctg atc cat	640
Val Thr Glu His Phe Arg Lys Lys Arg Ser Glu Tyr Tyr Leu Ile His	
170 175 180	
gtt ctt ggg act ctg tgg tac ctg cct ccc tta att gtg tcc ctg gcc	688
Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro Leu Ile Val Ser Leu Ala	
185 190 195	
tcc tac tct ttg ctc atc ttc tcc ctg ggg agg cac aca cgg cag atg	736
Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met	
200 205 210	
ctg caa aat ggg aca agc tcc aga gat cca acc act gag gcc cac aag	784
Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro Thr Thr Glu Ala His Lys	
215 220 225 230	
agg gcc atc aga atc atc ctt tcc ttc ttc ttt ctc ttc tta ctt tac	832
Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe Phe Leu Phe Leu Leu Tyr	
235 240 245	
ttt ctt gct ttc tta att gca tca ttt ggt aat ttc cta cca aaa acc	880
Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly Asn Phe Leu Pro Lys Thr	
250 255 260	
aag atg gct aag atg att ggc gaa gta atg aca atg ttt tat cct gct	928

Lys Met Ala	Lys Met Ile Gly Glu Val Met Thr Met Phe Tyr Pro Ala	
265	270	275
ggc cac tca ttt att ctc att ctg ggg aac agt aag ctg aag cag aca		976
Gly His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr		
280	285	290
ttt gta gtg atg ctc cgg tgt gag tct ggt cat ctg aag cct gga tcc		1024
Phe Val Val Met Leu Arg Cys Glu Ser Gly His Leu Lys Pro Gly Ser		
295	300	310
aag gga ccc att ttc tct tag		1045
Lys Gly Pro Ile Phe Ser *		
315		

<210> 356
 <211> 790
 <212> DNA
 <213> Homo sapiens

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 <222> (86)..(310)

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 <222> (1)...(790)
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gtttggtgct tctaattggtc ttcta atg gtc ctc ctg gaa ccc aag ccc tgg	112
Met Val Leu Leu Glu Pro Lys Pro Trp	
1 5	
ctg gaa ctg atg ctg ctg tgg tgg tca ggg ttc agt gag cag gag gaa	160
Leu Glu Leu Met Leu Leu Trp Trp Ser Gly Phe Ser Glu Gln Glu Glu	
10 15 20 25	
gga ctt ggt gtt tac ccc ttg ttt acc cct ttc ctt ggc ttc ctt cca	208
Gly Leu Gly Val Tyr Pro Leu Phe Thr Pro Phe Leu Gly Phe Leu Pro	
30 35 40	
tgc agg cca ccc tgt gac ccc gtg gtg gcc ccc tct gga acc aag agc	256
Cys Arg Pro Pro Cys Asp Pro Val Val Ala Pro Ser Gly Thr Lys Ser	
45 50 55	
tgc cga ctt cca gca gca cac aca gga tca gtg ctg ggg cca tct gtg	304
Cys Arg Leu Pro Ala Ala His Thr Gly Ser Val Leu Gly Pro Ser Val	
60 65 70	
cac tga ccaaagcctc tgctggcctc accagaccaa ggccagtgtg tgcttcaggg	360

His *
75

agccttggat cctccaggct gccaacagaa acaccggccc tctcggcagc agcccatcc 420
ttccaccctt gcaactgggtc ctgaaaagcc cattttgggg ccgttgctat ttagccaacc 480
tgccctccct tgctctcctg tgattttctca ctattccggc tgcagctcgc tgggagaaac 540
acttgagagt cttttgtgct ccacacccat gtacttaaaa taccaggcct ataggtcatt 600
tcaatgaggg aatttggctc ataacacgtg tgccccgagg cnagnatcct acttctgcag 660
atgctggcca agaagggtc tgtcccagcc gccatggggt ggggccacag agagggcagg 720
gccacgtgga gggcagagca tgtggctcct gtcagggtgcg cccattgctt nacttcagcc 780
cagtatcaag 790

<210> 357
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (67)..(246)

<400> 357
ggcatatttc aggtttcagt gacatagatc aagtaatttt aaaccaattt ggttattcta 60
tctaag atg agg gac atg gct att aag gtc aag cca aac tat act aaa 108
Met Arg Asp Met Ala Ile Lys Val Lys Pro Asn Tyr Thr Lys
1 5 10
agt agt ata ggg cag cag tta aaa tta tct ttt gaa aat caa gta tta 156
Ser Ser Ile Gly Gln Gln Leu Lys Leu Ser Phe Glu Asn Gln Val Leu
15 20 25 30
cct ggt ttc ttc tgt cac aac aga ata gct ggt tac cta gtc agt cac 204
Pro Gly Phe Phe Cys His Asn Arg Ile Ala Gly Tyr Leu Val Ser His
35 40 45
agt tgc cct tgc ctt ccc ttg tta gtc cct gga ggt act tga gtggaac 253
Ser Cys Pro Cys Leu Pro Leu Leu Val Pro Gly Gly Thr *
50 55 60
agaaggtaga attagcaaca gctcaatcac tttaggtagc atttctcctg aattctgctg 313
ccaaatcctc agggctctatg gattgggtga aatagtaaaa tcacacatag tgatttcttg 373
cacagcgtaa aggcgtttta ttttagtgta tagtgaacaa agaaggaaaa ctgggtcata 433

<210> 358
 <211> 1483
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (117)..(911)

<400> 358

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agttgattgc aggtcctcct ggggccagaa gggcgcctgg gaggccaggt tctggggatc      60

ccctccatcc agaagaacca cctgctcact ctgtcccttc gcctgctgct gggacc      116
atg ggg gct ggg gcc agt gct gag gag aag cac tcc agg gag ctg gaa      164
Met Gly Ala Gly Ala Ser Ala Glu Glu Lys His Ser Arg Glu Leu Glu
   1             5             10             15

aag aag ctg aaa gag gac gct gag aag gat gct cga acc gtg aag ctg      212
Lys Lys Leu Lys Glu Asp Ala Glu Lys Asp Ala Arg Thr Val Lys Leu
           20             25             30

ctg ctt ctg ggt gcc ggt gag tcc ggg aag agc acc atc gtc aag cag      260
Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln
           35             40             45

atg aag att atc cac cag gac ggg tac tcg ctg gaa gag tgc ctc gag      308
Met Lys Ile Ile His Gln Asp Gly Tyr Ser Leu Glu Glu Cys Leu Glu
           50             55             60

ttt atc gcc atc atc tac ggc aac acg ttg cag tcc atc ctg gcc atc      356
Phe Ile Ala Ile Ile Tyr Gly Asn Thr Leu Gln Ser Ile Leu Ala Ile
           65             70             75             80

gta cgc gcc atg acc aca ctc aac atc cag tac gga gac tct gca cgc      404
Val Arg Ala Met Thr Thr Leu Asn Ile Gln Tyr Gly Asp Ser Ala Arg
           85             90             95

cag gac gac gcc cgg aag ctg atg cac atg gca gac act atc gag gag      452
Gln Asp Asp Ala Arg Lys Leu Met His Met Ala Asp Thr Ile Glu Glu
           100            105            110

ggc acg atg ccc aag gag atg tcg gac atc atc cag cgg ctg tgg aag      500
Gly Thr Met Pro Lys Glu Met Ser Asp Ile Ile Gln Arg Leu Trp Lys
           115            120            125

gac tcc ggt atc cag gcc tgt ttt gag cgc gcc tcg gag tac cag ctc      548
Asp Ser Gly Ile Gln Ala Cys Phe Glu Arg Ala Ser Glu Tyr Gln Leu
           130            135            140

aac gac tcg gcg ggc tac tac ctc tcc gac ctg gag cgc ctg gta acc      596
Asn Asp Ser Ala Gly Tyr Tyr Leu Ser Asp Leu Glu Arg Leu Val Thr
           145            150            155            160

ccg ggc tac gtg ccc acc gag cag gac gtg ctg cgc tcg cga gtc aag      644
Pro Gly Tyr Val Pro Thr Glu Gln Asp Val Leu Arg Ser Arg Val Lys

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165	170	175	
acc act ggc atc atc gag acg cag ttc tcc ttc aag gat ctc aac ttc			692
Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp Leu Asn Phe			
180	185	190	
cgg atg ttc gat gtg ggc ggg cag cgc tcg gag cgc aag aag tgg atc			740
Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys Lys Trp Ile			
195	200	205	
cac tgc ttc gag ggc gtg acc tgc atc atc ttc atc gcg gcg ctg agc			788
His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Ile Ala Ala Leu Ser			
210	215	220	
gcc cta cga cat ggt gct agt gga gga cga cga agt gaa ccg cat gca			836
Ala Leu Arg His Gly Ala Ser Gly Gly Arg Arg Ser Glu Pro His Ala			
225	230	235	240
cga gag cct gca cct gtt caa cag cat ctg caa cca ccg cta ctt cgc			884
Arg Glu Pro Ala Pro Val Gln Gln His Leu Gln Pro Pro Leu Leu Arg			
245	250	255	
cac gac gtc cat cgt gct ctt cct taa caaga aggacgtctt cttcgagaag			936
His Asp Val His Arg Ala Leu Pro *			
260	265		
atcaagaagg cgcacctcag catctgtttc ccggactacg atggacccaa cacctacgag			996
gacgccggca actacatcaa ggtgcagttc ctcgagctca acatgcggcg cgacgtgaag			1056
gagatctatt cccacatgac gtgcgccacc gacacgcaga acgtcaaatt tgtcttcgac			1116
gctgtcaccg acatcatcat caaggagAAC ctcaaagact gtggcctctt ctgagcacca			1176
aatctttgct tatagatcca cagccagggc ctgtgctgca gtcggggaca aggagcttcc			1236
gtctggcaag ggaagctgag agccatggct gaactatcag ggacaaaggc ccatgtcccc			1296
acatccctgc tccctccttc ctcatccagc accaaatctt tgcttatgct ccacagccag			1356
ggcctgtgct gcagtcgggg acaaggagct tccgtactgg caaggccggg gcacaatttg			1416
cactcccctc agctagacgc acagactcag caataaacct ttgcatcagg caaaaaaaaa			1476
aaaaaaaa			1483

<210> 359
 <211> 714
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(441)

<400> 359

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Met Lys Pro Thr Leu Ile Ser Val Leu Val Ile Ile Phe Ile Leu Arg
1 5 10 15

gga aca aga gcc cag aga gtg act cag ccc gag aag ctc ctc tct gtc 96
Gly Thr Arg Ala Gln Arg Val Thr Gln Pro Glu Lys Leu Leu Ser Val
20 25 30

ttt aaa ggg gcc cca gtg gag ctg aag tgc aac tat tcc tat tct ggg 144
Phe Lys Gly Ala Pro Val Glu Leu Lys Cys Asn Tyr Ser Tyr Ser Gly
35 40 45

agt cct gaa ctc ttc tgg tat gtc cag tac tcc aga caa cgc ctc cag 192
Ser Pro Glu Leu Phe Trp Tyr Val Gln Tyr Ser Arg Gln Arg Leu Gln
50 55 60

tta ctc ttg aga cac atc tct aga gag agc atc aaa ggc ttc act gct 240
Leu Leu Leu Arg His Ile Ser Arg Glu Ser Ile Lys Gly Phe Thr Ala
65 70 75 80

gac ctt aac aaa ggc gag aca tct ttc cac ctg aag aaa cca ttt gct 288
Asp Leu Asn Lys Gly Glu Thr Ser Phe His Leu Lys Lys Pro Phe Ala
85 90 95

caa gag gaa gac tca gcc atg tat tac tgt gct cta agt ggc aca gta 336
Gln Glu Glu Asp Ser Ala Met Tyr Tyr Cys Ala Leu Ser Gly Thr Val
100 105 110

gct ggt ttt gca agg aag cag aac aca aac cct tta aat aca gga aat 384
Ala Gly Phe Ala Arg Lys Gln Asn Thr Asn Pro Leu Asn Thr Gly Asn
115 120 125

att tct ttg caa act ctc tgt atg gcc aca gca ggg cat tct ttc tcc 432
Ile Ser Leu Gln Thr Leu Cys Met Ala Thr Ala Gly His Ser Phe Ser
130 135 140

aga aat taa tattgag tttatctcgt agatattata tcatcactca tcagctagcc 488
Arg Asn *
145

atacaccac ctcacaattt tgtccaaaaa attctcatca tttaccctgc ctaaattaaa 548

tttaaaaata gtaaacgtat tcatttcgtc tagcagcact ggacacacac cttcgaaata 608

aaaactacct tgcactgcac aaaaaacaaa aacaaaaaca cattgccggc cgccccctta 668

ttcccctcag tcagggtac cctaccttcc acctcatccg ctcatt 714

<210> 360

<211> 3154

<212> DNA

<213> Homo sapiens

<220>
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 <222> (278)..(1483)

<400> 360

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aactgcttcg cctggtcggc cgcgcacccg ccggtctagc gaactgggtg atcatgacct	120
ggtgccgcag ctcgtccatg ttcaccgaca tggcgcggcc gcgcggggcc cggcgtctcc	180
ggccggacgc agacgcgggg ctgcgctcgt agcggggccc cggatccccg agtggcggcc	240
ggagcctcga aaagagattc tcagcgtga ttttgag atg atg ggc ttg gga aac	295
Met Met Gly Leu Gly Asn	
1 5	
ggg cgt cgc agc atg aag tgc ccg ccc ctc gtg ctg gcc gcc ctg gtg	343
Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val Leu Ala Ala Leu Val	
10 15 20	
gcc tgc atc atc gtc ttg ggc ttc aac tac tgg att gcg agc tcc cgg	391
Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp Ile Ala Ser Ser Arg	
25 30 35	
agc gtg gac ctc cag aca cgg atc atg gag ctg gaa ggc agg gtc cgc	439
Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly Arg Val Arg	
40 45 50	
agg gcg gct gca gag aga ggc gcc gtg gag ctg aag aag aac gag ttc	487
Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys Asn Glu Phe	
55 60 65 70	
cag gga gag ctg gag aag cag cgg gag cag ctt gac aaa atc cag tcc	535
Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser	
75 80 85	
agc cac aac ttc cag ctg gag agc gtc aac aag ctg tac cag gac gaa	583
Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu	
90 95 100	
aag gcg gtt ttg gtg aat aac atc acc aca ggt gag agg ctc atc cga	631
Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg	
105 110 115	
gtg ctg caa gac cag tta aag acc ctg cag agg aat tac ggc agg ctg	679
Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu	
120 125 130	
cag cag gat gtc ctc cag ttt cag aag aac cag acc aac ctg gag agg	727
Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg	
135 140 145 150	
aag ttc tcc tac gac ctg agc cag tgc atc aat cag atg aag gag gtg	775
Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu Val	
155 160 165	

aag gaa cag tgt gag gag cga ata gaa gag gtc acc aaa aag ggg aat	823
Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys Gly Asn	
170 175 180	
gaa gct gta gct tcc aga gac ctg agt gaa aac aac gac cag aga cag	871
Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp Gln Arg Gln	
185 190 195	
cag ctc caa gcc ctc agt gag cct cag ccc agg ctg cag gca gca ggc	919
Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu Gln Ala Ala Gly	
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Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly Asn Val Leu Gly Asn	
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Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu Val Val Leu Asp Ser	
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Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu Ile Gln Val Val Asn	
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Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu Pro Gly Arg Glu Gln	
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Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly Phe Gly Gly Ala Gly	
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Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala Leu Ser Val Ser Gln	
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Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro	
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Asp Gly Gln Glu Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln	
330 335 340	
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Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala	
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Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn	
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Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	
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Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu *	
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Tyr Cys Ile Tyr Ile Leu Val Leu Tyr Ile Asn His Lys Ile Phe Ser
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Pro His Cys Ser Ile Ala Leu Arg Glu Ile Pro Cys Lys Pro Leu Leu
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Ser Thr Lys Leu *
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Ser Phe Leu Trp Gln Asn Gln Asp Glu Glu Thr Ser Cys Gly Asp Leu	
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His Ile Val Trp Thr Tyr Asn Thr Thr Ser Ala Val Thr Val Lys Ser	
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Thr Ile Arg Arg Leu Lys Gln Leu Lys Asp Gln *	
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